US008546078B2

(12) **United States Patent**
Freije et al.

(10) **Patent No.: US 8,546,078 B2**
(45) **Date of Patent: *Oct. 1, 2013**

(54) MATERIALS AND METHOD FOR ASSAYING FOR METHYLATION OF CPG ISLANDS ASSOCIATED WITH GENES IN THE EVALUATION OF CANCER

(75) Inventors: **Wadiha Freije**, Forest Park, IL (US); **Deborah Nusskern**, Forest Park, IL (US)

(73) Assignee: **Euclid Diagnostics LLC**, Crown Point, IN (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 74 days.

This patent is subject to a terminal disclaimer.

(21) Appl. No.: **12/983,738**

(22) Filed: **Jan. 3, 2011**

(65) **Prior Publication Data**

US 2011/0097728 A1 Apr. 28, 2011

Related U.S. Application Data

(60) Division of application No. 12/115,674, filed on May 6, 2008, now abandoned, which is a continuation of application No. PCT/US2006/060685, filed on Nov. 8, 2006.

(60) Provisional application No. 60/734,577, filed on Nov. 8, 2005.

(51) **Int. Cl.**
C12Q 1/68 (2006.01)

(52) **U.S. Cl.**
USPC **435/6.1**; 435/6.11; 435/6.12; 435/6.14

(58) **Field of Classification Search**
None
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

6,251,594	B1	6/2001	Gonzalgo et al.	
2003/0198972	A1	10/2003	Erlander et al.	
2005/0064414	A1	3/2005	Hanna	
2005/0196792	A1	9/2005	Fodor et al.	
2005/0214812	A1	9/2005	Li et al.	
2006/0024676	A1	2/2006	Uhlmann et al.	
2007/0026393	A1*	2/2007	Berlin et al.	435/6
2007/0059720	A9	3/2007	Fuqua et al.	

FOREIGN PATENT DOCUMENTS

WO	WO 97/046705	A1	12/1997
WO	WO 00/060085	A1	10/2000
WO	WO 00/070090	A1	11/2000
WO	WO 02/00928	A2	1/2002
WO	WO 03/044232	A1	5/2003
WO	WO 2004/067775	A2	8/2004
WO	WO 2005/005660	A1	1/2005
WO	WO 2005/007830	A2	1/2005
WO	WO 2005/042713	A2	5/2005
WO	WO 2005/054517	A2	6/2005

OTHER PUBLICATIONS

Cairns et al., *Clin. Cancer Res.*, 7: 2727-2730 (2001).
Clark et al., *Nucleic Acids Research*, 22(15): 2990-2997 (1994).
Derks et al., *Cellular Oncology*, 26(5/6): 291-299 (2004).
Dunn et al., *Journal of Pathology*, 203: 672-680 (2004).
El-Maarri et al., *Nucleic Acids Research*, 30(6): e25, pp. 1-4 (2002).
Esteller et al., *Cancer Research*, 61: 3225-3229 (2001).
Falls, Douglas, *Experimental Cell Research*, 284(1): 14-30 (2003).
Fernandez et al., #1590, *Proc. of the American Association for Cancer Research*, 47: pp. 375 (Apr. 2006).
Frommer et al., *Proc. Natl. Acad. Sci. USA*, 89: 1827-1831 (Mar. 1992).
Goessl et al., *Ann. N.Y. Acad. Sci.*, 945: 51-58 (2001).
Gonzalgo e al., *Clin. Cancer Res.*, 9: 2673-2677 (2003).
Grossfeld et al., *Epidemiol. Rev.*, 23(1): 173-180 (2001).
Herman et al., *Proc. of the Natl. Acad. Sci. USA*, 93: 9821-9826 (Sep. 1996).
Hesson et al., *Oncogene*, 22: 947-954 (2003).
Huang et al., *Cancer Research*, 64(19): 6840-6844 (Oct. 1, 2004).
Humphrey et al., *J. Urol.*, 155: 816-820 (1996).
Jeronimo et al., *Urology*, 60: 1131-1135 (2002).
Laird, Peter, *Human Molecular Genetics*, 14(Rev. Issue 1): R65-R-76 (2005).
Lerman et al., *Cancer Research*, 60: 6116-6133 (Nov. 1, 2000).
Li et al., *Biochimica et Biophysica Acta*, 1704: 87-102 (2004).
Mettlin et al., *Cancer*, 82(2): 249-251 (1998).
Mettlin et al., *Cancer*, 83(8): 1679-1684 (1998).
Olek et al., *Nucleic Acids Research*, 24(24): 5064-5066 (1996).
Schulz et al., *J. Cell. Mol. Med.*, 10(1): 100-125 (2006).
Singal et al., *Blood*, 93(12): 4059-4070 (1999).
Takai et al., *Proc. Natl. Acad. Sci.*, 99(6): 3740-3745 (2002).
Thompson et al., *N. Engl. J. Med.*, 350: 2239-2246 (2004).
European Patent Office, Extended European Search Report in European Application No. 10153479.0-2402 (Dec. 20, 2010).
European Patent Office, International Search Report for International Patent Application No. PCT/US2006/060685 (Nov. 16, 2007).

* cited by examiner

Primary Examiner — Hong Sang
(74) *Attorney, Agent, or Firm* — Leydig, Voit & Mayer, Ltd.

(57) **ABSTRACT**

Provided are methods, reagents, and kits for evaluating cancer, such as prostate cancer, in a subject. Disclosed methods of evaluating cancer include methods of diagnosing cancer, methods of prognosticating cancer and methods of assessing the efficacy of cancer treatment. The methods include assaying a biological sample for methylation of a CpG island associated with specified genes. Provided reagents and kits include primers suitable for amplifying at least a portion of a target CpG islands associated with specified genes.

24 Claims, 67 Drawing Sheets

FIG 1A

GAGTTTATTTTCGTTTGCGTGCGATAGGGTTTTTGTATTTAAGTGAGTTAA
GGAATGAATTTCGAATTTTTTTGGGAAAGTTATTAACGTTTTTTTCGTATTT
TTTTTAGGGTTTTTGATTACGGAGATTTTGTTTGGGGTATAGGTGTGGGAG
TCGTAAATTTTTTTTTGCGTCGTTTTTTTTCGCGTGGAATGGGACGGAGTA
GTTTTTTTAGGCGTTGTTTGGTTGCGGAGGGGAGCGGGTAGCGAGAGTTT
CGGGTTTTCGTTTGGGTTTTCGGGTTTTCGGGGCGTTGGTTTCGGTTTTCGC
GTAGCGTTTAGCGATTTTTGTCGGGGGTTTTCGGTAGTCGCGTCGTTATTT
TTCGTTCGGTTAGCGCGGGAGGAAAAGGGGTTGCGTTCGGGAGCGTCGAG
TTTAGGTTTTTTTCGGTGGCGTGTTCGCGTTTCGGGGTGGGGGTGTGGTGG
GGAAGAGGGAGGGGGCGAGGTTAGGGGAGGGTGCGAAGGAGGCGTTTGT
TTTTAATTTGCGGGCGGGAGGTGGGTGGTTGCGGGGTAATTGAAAAAGAG
TCGGCGAGGAGTTTTTCGAAATTTGTTGGAATTTCGGGTTCGCGCGGAGG
TTAGGAGTTGAGCGGCGGCGGTTGTCGGACGATGGGAGCGTGAGTAGGA
CGGTGATAATTTTTTTTCGATCGGGTTGCGAGGGCGTCGGGTAGAGGTTA
GGACGCGAGTCGTTAGCGGTGGGATTTATCGACGATTTTTCGGGGCGATA
GGAGTAGTTTCGAGAGTTAGGGCGAGCGTTCGTTTTAGGTGGTCGGATCG
TTCGTCGCGTTCGCGTCGCGTTTTTTGTAGGTAACGGGAGACGTTTTCGCG
TAGCGCGAGCGTTTTAGCGCGGTCGTTCGTTTTTTTTTTCGAGGGATAAAT
TTTTTTTAAATTCGATTCGAGTTTTTGGATTAAATTCGTTTGCGTCGAGAGT
CGTTCGCGTAGAGCGTTTCGTTTTCGGCGAGATGTTCGAGCGTAAAGAAG
GTAGAGGTAAAGGGAAGGGTAAGAAGAAGGAGCGAGGTTTCGGTAAGAA
GTCGGAGTTCGCGGCGGGTAGTTAGAGTTTAGGTGGGTGCGTAGCGCGGT
TCGGGTTTTACGATTTTTTTTTTGTTTTTTTTATTTTTTTTTTTTTTCGGATGT
CGTGGTTTTTTTTTTTTTTTTTTTTTCGTTCGTTTTTTTCGTTTTGCGTTTTGA
GCGTTCGTTGAGTCGCGCGGTGTTTTTTTTTTTGGGGGTCGTCGTTTATTG
GGCGTCGAGTTTTATCGGGCGTTTACGTTTAGAGTTTAGGGTAAGGGATA
GTAGTTTCGGTCGTATTTTTTTAGAGTTTCGGGAGCGTTTCGTTTTTTGGTA
CGGTTTTTTTTTAGCGTTTTAGCGGTTGAGTTTAGTTCGGGAGTGGGATTT
GGGTTATAGGAGTCGAGGTTGCGTGCGCGCGTGTTTCGCGTTATAAGCGT
TTTGTACGGGGGTCGTGTGTTTTTTAGCGGGAAACGTTGGAATGGGTCGTT
TGGAGGGAGAGTCGGTTTTTTCGGTGTGTTTGGTAGCGTAGAAGTGGGTG
GTCGAGTAAGAGGTCGCGTGGGAAGT
[SEQ ID NO: 1]

FIG 1B

ATTTTTTACGCGGTTTTTTGTTCGATTATTTATTTTTGCGTTGTTAGGTATA
TCGAGGGGATCGGTTTTTTTTTTAGGCGGTTTATTTTAGCGTTTTTCGTTAG
AGGGTATACGGTTTTCGTGTAAAGCGTTTATGGCGCGGGGTACGCGCGTA
CGTAGTTTCGATTTTTATAGTTTAGGTTTTATTTTCGGGTTGGGTTTAGTCG
TTAAGGCGTTGGGGAGGGGTCGTGTTAGGGAGCGAAGCGTTTTCGGGATT
TTGGGAGGGTGCGGTCGGGATTGTTGTTTTTTGTTTTGAGTTTTGGGCGTA
GGCGTTCGGTAGGATTCGGCGTTTAGGTGAGCGGCGGTTTTTAGGAGGGG
AAGTATCGCGCGATTTAACGGGCGTTTAGAGCGTAGGGCGAAGAGGACG
GGCGAGGGAGAGGGGGAGGGAGAGGTTACGGTATTCGAGGAGGAGGAG
GAGTAGGAGGAGTAGGAGGAGGATCGTGGGGTTCGGGTCGCGTTGCGTA
TTTATTTGGGTTTTGGTTGTTCGTCGCGGATTTCGGTTTTTTGTCGGAGTTT
CGTTTTTTTTTTTTGTTTTTTTTTTTGTTTTTGTTTTTTTTGCGTTCGGATATT
TCGTCGGAGACGGAGCGTTTTACGCGGACGGTTTTCGGCGTAGGCGAGTT
TGGTTTAAGGGTTCGGATCGGGTTTGGGAAAAGTTTGTTTTTCGAGGGGG
AGAGCGAGCGGTCGCGTTGAGGCGTTCGCGTTGCGCGGGGGCGTTTTTCG
TTGTTTGTAGGGAGCGCGGCGCGGACGCGGCGGGCGGTTCGGTTATTTGG
AACGGGCGTTCGTTTTGGTTTTCGGGGTTGTTTTTGTCGTTTCGGGAAGTC
GTCGATGGGTTTTATCGTTGGCGGTTCGCGTTTTGGTTTTTGTTCGGCGTTT
TCGTAATTCGATCGGGGAGAGGTTATTATCGTTTTGTTTACGTTTTTATCG
TTCGGTAGTCGTCGTCGTTTAGTTTTTGGTTTTCGCGCGAGTTCGGAGTTTT
AATAAGTTTCGGGGAATTTTTCGTCGGTTTTTTTTTAATTGTTTCGTAGTTA
TTTATTTTTCGTTCGTAGGTTGGAGGTAGGCGTTTTTTTCGTATTTTTTTTT
GGTTTCGTTTTTTTTTTTTTTTTTTTATTATATTTTTATTTCGAGGCGCGGATAC
GTTATCGGGAGGAGTTTGGGTTCGGCGTTTTCGGGCGTAGTTTTTTTTTTTT
TCGCGTTGGTCGGGCGGGGGGTGGCGGCGCGGTTGTCGGGAATTTTCGAT
AGGGGTCGTTGGACGTTGCGCGGAGATCGAGGTTAGCGTTTCGGAGATTC
GGGAATTTAGGCGGAGATTCGAGGTTTTCGTTGTTCGTTTTTTTTCGTAGT
TAGGTAGCGTTTGGGAGGGTTGTTTCGTTTTATTTTACGCGGAAAAGGAC
GGCGTAGAGAAAAGTTTGCGATTTTTATATTTGTGTTTTAAGTAGAGTTTT
CGTGGTTAGGAATTTTGGGAGGGGTGCGGGGGGAACGTTGGTGGTTTTTT
TAGAAGAGTTCGGGGTTTATTTTTTAATTTATTTAAGTATAAAAGTTTTGT
CGTACGTAGGCGAAAATAAATTT
[SEQ ID NO: 2]

FIG 1C

ATTTTGGCGTTTAATATCGTTAATATTAGTGGGTTGTTAGGGGTTTCGTGG
GAGGCGGTTTTAGTCGGGGTTTTGTTGGCGTTGGCGGTGTTGGTTATCGTG
GGAGGTAATTTGTTGGTTATCGTGGTTATCGTTTGGATTTCGAGATTTTAG
ATTATGATTAACGTGTTCGTGATTTCGTTGGTCGTAGTCGATTTGGTGATG
GGATTTTTGGTGGTGTCGTCGGCGGTTATTTTGGCGTTGATTGGTTATTGG
TCGTTGGGCGTTATTGGTTGCGAGTTGTGGATTTCGGTGGACGTGTTGTGT
GTGATCGTTAGTATCGAAATTTTGTGCGTTTTGGTCGTGGATCGTTATTTG
GTTGTGATTAATTCGTTGCGTTACGGCGTATTGGTTATTAAGCGTTGCGTT
CGGATAGTTGTGGTTTTGGTGTGGGTCGTGTCGGTCGCGGTGTCGTTTGCG
TTTATTATGAGTTAGTGGTGGCGCGTAGGGGTCGACGTCGAGGCGTAGCG
TTGTTATTTTAATTCGCGTTGTTGTGTTTTCGTTTTTAATATGTTTTACGTGT
TGTTGTTTTTTTTCGTTTTTTTTTATTTTTTTTTTTTCGTGATGTTTTTCGTTT
ACGCGCGGGTTTTCGTGGTGGTTACGCGTTAGTTGCGTTTGTTGCGCGGGG
AGTTGGGTCGTTTTTCGTTCGAGGAGTTTTCGTCGGCGTCGTCGCGTTTTTT
GGTTTCGGTTTCGGTGGGGACGTGCGTTTCGTTCGAAGGGGTGTTCGTTTG
CGGTCGGCGGTTCGCGCGTTTTTTGTTTTTTCGGGAATATCGGGTTTTGTG
TATTTTGGGTTTTATTATGGGTATTTTTATTTTTTGTTGGTTGTTTTTTTTT
TGGTTAACGTGTTGCGCGTTTTGGGGGGTTTTTTTTTAGTTTCGGGTTCGGT
TTTTTTTGTTTTGAATTGGTTAGGTTATGTTAATTTTGTTTTTAATTCGTTTA
TTTATTGTCGTAGTTCGGATTTTCGTAGCGTTTTTCGTCGTTTTTTGTGTCG
TTGCGGTCGTCGTTTGTTTTCGGAGTTTTGCGTCGTCGTTCGTTCGGTTTTT
TTTTTTTCGGGCGTTTTTGCGGTTCGGAGTAGTTTAGCGTAGTTTAGGTTTT
GTTAACGGTTCGACGGGTAGGTAATCGGGGTAGAGGGATCGGCGGTTTAG
GGTCGGGAAGTATGCGATGTGTTCGTGGGTTAATTTTTTGAGTGTGGAGTT
TATTAAGAGAAGGTGGGATGGTTTTGTTTGGAGAGAAAAGGGAACGAGG
AGTAGCGAATTAAAATGGGATTTAGGGTTTTTTTTTTTTCGGATTTAGTTA
TTAGGGTAGAAGTA
[SEQ ID NO: 3]

FIG 1D

TGTTTTTATTTTAGTGATTGGATTCGGAAAGAAAAGGATTTTGGGTTTTAT
TTTGGTTCGTTATTTTTCGTTTTTTTTTTTTTTTAAGTAAAGTTATTTTATTT
TTTTTTAATAAATTTTATATTTAAAAAGTTGATTTACGGATATATCGTATG
TTTTTCGATTTTGAGTCGTCGGTTTTTTTGTTTCGGTTATTTATTCGTCGAG
TCGTTGGTAAAGTTTGGGTTGCGTTGGGTTGTTTCGGGTCGTAGGAACGTT
CGAGGGGAAGAGGGTCGGGCGGGCGGCGGCGTAGGGTTTCGGAGGTAGG
CGACGGTCGTAGCGGTATAGAAGACGGCGGAAGGCGTTGCGAAAGTTCG
GGTTGCGGTAGTAGATGAGCGGGTTGAAGGTAGAATTGGTATAATTTAGT
TAGTTTAGGGTAAGGAAAGTCGGGTTCGGGATTAGAGAGGGGTTTTTTAG
GGCGCGTAGTACGTTGGTTAGAAAGAAGGGTAATTAGTAGAGAGTGAAG
GTGTTTATGATGAGATTTAAGGTGTATAGGGTTCGGTGTTTTCGGAGAGGT
AGGAGGCGCGCGGGTCGTCGGTCGTAGGCGGGTATTTTTTCGGGCGGAGC
GTACGTTTTTATCGGGGTCGGGGTTAGAGAGCGCGACGGCGTCGGCGGAG
ATTTTTCGGGCGGAAAGCGGTTTAGTTTTTCGCGTAGTAAGCGTAGTTGGC
GCGTAGTTATTACGAAAATTCGCGCGTAGACGAAGAGTATTACGAGAAGA
GGAAGGTAGAAGGAGACGGAGGAGGATAGTAGTACGTAGGGTATGTTGG
AGGCGAAGGTATAGTAGCGCGGGTTGGAGTGGTAGCGTTGCGTTTCGGCG
TCGGTTTTTACGCGTTATTATTGGTTTATGATGGGCGTAAACGATATCGCG
GTCGATACGATTTATATTAGGATTATAGTTGTTCGGGCGTAGCGTTTGGTG
ATTAGTGCGTCGTAACGTAGCGGGTTGGTTATAGTTAGGTAGCGGTTTAC
GGTTAGGGCGTATAGGGTTTCGATGTTGGCGGTTATATATAGTACGTTTAT
CGAGGTTTATAGTTCGTAGTTAGTGGCGTTTAACGGTTAGTGGTTAGTTAG
CGTTAAGGTGGTCGTCGGCGGTATTATTAGGAGTTTTATTATTAGGTCGGT
TGCGGTTAGCGAAGTTACGAATACGTTGGTTATGGTTTGGAGTTTCGGAG
TTTAGGCGATGGTTACGATGATTAGTAGGTTGTTTTTTACGGTGGTTAGTA
TCGTTAGCGTTAGTAGGGTTTCGGTTAGGGTCGTTTTTTACGGAATTTTTG
GTAGTTTATTGGTGTTGGCGGTATTGGGCGTTAGGGT
[SEQ ID NO: 4]

FIG 1E

CGAAAAGTTTTTGAGGCGTTGCGTGTATTTTATTTTAGGATATCGTGTGTG
CGCGTCGAGTTGAGTGCGAGGAACGTGGCGCGAGGGTCGGGGGATGTCG
GGTTGCGTGGGTGTGAGTTTTCGCGCGATCGCGATTTCGCGTTTTTTTCGT
TTTCGTCGGAACGTGATCGTAGTCGTATTTTTTTTTTAGTTTTTTTTTAGTT
AGACGTTTTTTTTTAGGTTTTTTTGGGCGTTTATTGTAAATTTTGCGATTAA
AATACGTCGGTGAGTTCGGTTTATCGATAGATGGATTAATCGTTTTTTTTT
CGGTTAGGGGAGGAGGAATTTTTTAATTTCGGAGTTTAGGGAGTCGGGAG
TTGTTTCGGGACGAGTTTTTCGGAGTTTAGTCGGTTGCGGAGTTTCGGTTC
GGGTCGGTTTCGGGGTTTTTTTGTCGGGGTGGGGTGCGAGTTTTTGTTCGA
TTTTTTTGGGGCGGTTTAGGTAGGTTTGTCGGTTTTCGAGGAGGTGGTTAG
GGCGTTTTGGTTTAGTAGGTTTTTTTTCGAGTCGGGGGGAGGGGAGATCG
GTTGGGGAAGGGGTATTTCGAAGGGGTGGAGGTCGGGGCGGGCGGGAGG
TAAGCGCGTCGCGGGCGTGAGGGTAAAGTTTTCGAGGTTCGCGCGGAGAG
TATACGTGTATGTGCGCGCGGGGTTAGGTCGGGGTCGGTAGGATGCGTTG
GGTTCGGGGGCGCGCGGGGTCGGCGTCGAAGGGGATAATTTTTTTTTTG
GTATTATCGGGGAGACGTTTTGTCGGTTTCGGTTTTTGGGCGTAGGGACGT
TTTAGTTTACGGAGGGTGGAGTTTTTTTTAGATTCGGGTTATCGGTTGGGG
TTTTTTTAACGTTTTGTTTTTCGAGTTTTCGGATGGTTCGGGTTTTACGGAT
TTCGCGTTTTTTAGTTTTAGTTTAGTTTTTTAGGTTTTTTAGATTTAGCGGC
GTAGGGGGCGGGGGTAGGGGTAGTGGGGGTTGGAGGGCGTAGTCGGTTT
TTAGGGTGGGGAGAGTTGCGGGGGGAGGAGGAGGAGGGTGTCGACGTTT
GAGTGGGTTCGAGTTCGAGTCGTAGTCGGGGGAGTTAGTTAGTTTTCGGT
TAAGGTAGTAGGTTAGTTTTAGGAAGGGCGGGCGATTGAGTCGAGGGAGT
CGGCGGTTGGGTTTTTTTTTCGGTTCGCGATTTTCGGCGTCGTCGTCGTCGT
TATCGTTATCGTTATCGTTTTCGTTTTGTCGTCGTCGTCGTTGTAGAGTATC
GTAGTTTCGTCGCGTTTTCGCGTTTCGCGTTTCGCGTCGTTAGTCGTTTGGG
AGTTCGAGCGTCGAGTTCGGGGCGGAGGAGAGGGGCGTTGGCGCGAGAG
TTCGGGCGAGGGAGTCGCGAAGGGAGAAGGGGGCGGGCGGAGGGAGGA
GTAGGGAGAGTGGGAGAAGGGGGAGGGAGAGAGGAGAGCGAGGGAGAG
TTGGAGAGAGCGAGAGTAAAGAGCGAGCGAGGGAGAGGAGAGAGAGAG
AGAGGAGAGAGAAAGATATACGTACGTAGAGATATACGGTTATTGGAAT
TTTATTAGAAAAAAGTGAGTCGAGTAAGGGTTAGCGGGAG
[SEQ ID NO: 5]

FIG 1F

TTTTCGTTAATTTTTGTTCGGTTTATTTTTTTTTAATGGAATTTTAGTGATC
GTGTGTTTTTGCGTGCGTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
TTCGTTCGTTTTTTGTTTTCGTTTTTTTTAGTTTTTTTTCGTTTTTTTTTTTTT
GCGGTTTTTCGTTCGGGTTTTCGCGTTAGCGTTTTTTTTTTTTCGTTTCGGG
TTCGGCGTTCGGGTTTTAGGCGGTTGGCGGCGCGGGGCGCGGGGCGCGG
GAGCGCGGCGGAGTTACGATGTTTTGTAGCGGCGGCGGCGATAAGGCGA
AGGCGGTGGCGGTGGCGGTGGCGGCGGCGGCGTCGGGGATCGCGGG
TCGAGAGGAGAGTTTAGTCGTCGGTTTTTTCGGTTTAATCGTTCGTTTTTTT
TGGGATTGATTTGTTGTTTTGGTCGGAAATTGATTGGTTTTTTCGGTTACG
GTTCGGGTTCGAATTTATTTAAGCGTCGGTATTTTTTTTTTTTTTTTTTCGT
AGTTTTTTTTATTTTGGGGATCGGTTGCGTTTTTTAATTTTTATTGTTTTTGT
TTTCGTTTTTTGCGTCGTTGGGTTTGGGAAGTTTGGGGAGTTGAGTTGAGG
TTGGAGGGCGCGGAGTTCGTGGGGTTCGAGTTATTCGGGGGTTCGGGGGG
TAGGGCGTTAGAAAAATTTTAGTCGGTGGTTCGGGTTTGAGGGGGGTTTT
ATTTTTCGTGGGTTAAGGCGTTTTTGCGTTTAGGAGTCGAGGTCGATAAAG
CGTTTTTTCGATGGTGTTAGGGAAAGGAATTATTTTTTTCGGCGTCGGTTT
CGCGCGTTTTCGAATTTAACGTATTTTGTCGGTTTCGGTTTAGTTTCGCGC
GTATATATACGTGTGTTTTTCGCGCGGATTTCGGGAATTTTGTTTTTACGTT
CGCGGCGCGTTTGTTTTTCGTTCGTTTCGGTTTTTATTTTTTCGAGATGTTT
TTTTTTTAGTCGGTTTTTTTTTTTTTCGGTTCGGGAAGAAGTTTGTTGGGTT
AGGGCGTTTTGATTATTTTTTCGGAGGTCGGTAAATTTGTTTGAATCGTTT
TAGAGGAATCGGGTAGGGGTTCGTATTTTATTTCGGTAGGAGGGTTTCGA
GATCGATTCGGGTCGGGGTTTCGTAGTCGGTTGGGTTTCGAGGAGTTCGTT
TCGAGGTAGTTTTCGGTTTTTTAGGTTTCGGGGTTGGGGGGTTTTTTTTTTT
TTAGTCGGGAAGGGGGCGATTGATTTATTTGTCGGTGGGTCGGGTTTATC
GGCGTGTTTTAGTCGTAGAATTTATAATAAACGTTTAGAAGGATTTAAAA
GGAAGCGTTTGGTTGGGAAAGGGTTGGAGGAGAGGTGCGGTTGCGGTTA
CGTTTCGGCGAGAGCGGGAGAGGCGCGGGGTCGCGGTCGCGCGAGGGTT
TATATTTACGTAGTTCGGTATTTTTCGGTTTTCGCGTTACGTTTTTCGTATT
TAGTTCGGCGCGTATATACGGTGTTTTGGGGTGGGGTATACGTAGCGTTTT
AGAAATTTTTCG
[SEQ ID NO: 6]

FIG 1G

GAGGTATTAGTTTTTGAAGGTTTATTTTTTAATATTGGTTGCGAGAGTAAG
AATGGTGTGTAATTTATAAAAGTCGTTATTGTTGTAGGTAAGTTGTAGTAA
ACGATTCGCGTTCGAGTATTTTCGTTTTCGTTTTCGTTGCGGTTTCGTTTAC
GACGATTTTGGGGAATTATAAGTTTCGTTATATAGCGGGGAGCGTTCGGA
GTTCGCGTCGGTTTCGTTTTTAGTTCGGTTTTTATTTTCGGTTTCGTTTTCG
GTTTTTTTTCGTCGGGTTAATTTCGAAGAGTCGTCGGTGGTCGCGGTAGAC
GGAAGTCGAACGAGTTTTTCGGCGGTTGTAGGATGGGGGATTTTAAAGTG
AAAGTGGCGGTGCGGATACGATTTATGAATCGGCGAGGTGAGAGTCGAG
TTTTTTGGGTCGTCGGGGCGGAGGCGGTAGGTGTTTGGCGCGTTTTTTTT
TCGGTCGTCGTGGGGGGTTCGGCGGTTTCGTTTTTATAGTTAGCGGCGGGG
CGCGAGGAGGGGTTCGGGGATTTTGAAATTCGTTTTCGCGTTGAGACGTT
CGGTTTTTTTTTTTTTTTTTTTTTTTTGGTTAGTTTCGTTTTTGGCGTCG
TCGGGTTTTTCGTGTCGGTTTCGTTGTTTTTTTCGTTTGCGTTCGTTTCGTTT
TTGCGTTTTTTTGTTTTTTCGTTTTTTTCGGAGGTTTTCGAGGGCGTTTTCG
GTTTTCGCGTTTAGTTTCGTTTTGGTTTTTTAGTTTCGTTTTTTTTTCGTTAG
TTGTTATCGTCGTTTTCGCGCGCGGGTCGTTAGTTTTTGTAGTTCGTTTCGG
GATCGTTCGGGATTTTTCGGGATTTCGCGTTTCGTTCGGGTCGTTTAAGTT
TGTATCGTTTTGGTTCGCGGCGGGAAGAAGGGTAGGGGGTTAGGCGGGTG
TTTCGCGGCGAGTTTTTTTTATTTGGGCGTTTTGAGATTGGGGTTAGGTGG
AGGAGATGTTTTTTTCGTTGTTTTTGGATAGTTGAGAAAGTTTTGGTTTTGT
TTGAAGTTTTATTTATTATTTTTTAATAAATAGTTAAAGTGTTAAGATTTTT
GTGGAATTGTATTTTTTTGATA
[SEQ ID NO: 7]

TGTTAGAAAGATATAATTTTATAAGAATTTTGGTATTTTAGTTATTTATTG
AGAGATGATGAATGAGATTTTAGGTAAAATTAAAATTTTTTTAATTGTTTA
AAAATAACGAAAAGGGTATTTTTTTTATTTGATTTTAATTTTAGGACGTTT
AGGTGGAAGGAATTCGTCGCGGGGTATTCGTTTGGTTTTTTGTTTTTTTTTT
CGTCGCGGGTTAAGGCGGTGTAGGTTTGGGCGATTCGGGCGAGACGCGGG
GTTTCGGGGGGTTTCGGGCGGTTTCGAGGCGGGTTGTAGGGGTTGGCGAT
TCGCGCGCGGGGGCGACGATGATAGTTGGCGGGGAAGGAGCGAGGTTGA
GGGGTTAGGACGAGGTTGGGCGCGAGGGTCGAGGGCGTTTTCGGGAATTT
TCGGGGGAGACGAGAGGGTAAAAGGGCGTAGGGGCGGGGCGGGCGTAG
GCGGAAGGGGTAGCGGGGTCGGTACGAGGGGTTCGACGGCGTTAGGGAC
GGGGTTGGTTAGGGGGGAAGGGAGGGGAGAAGAGGGAGTCGGGCGTTTT
AGCGCGGGAGCGGGTTTTAGGGTTTTCGGGTTTTTTTCGCGTTTCGTCGT
TGATTATAGGGGCGGGGTCGTCGGATTTTTTACGGCGGTCGAGGGAAGGG
CGCGTTAGGTATTTGTCGTTTTCGTTTCGGCGGTTTAGGAGGGTTCGGTTT
TTATTTCGTCGGTTTATGGGTCGTATTCGTATCGTTATTTTTATTTTGGAGT
TTTTTATTTTGTAGTCGTCGAGGAATTCGTTCGGTTTTCGTTTGTCGCGGTT
ATCGGCGATTTTTCGGGGTTGATTCGGCGGGAGGGGGTCGGGGGCGGAGT
CGGGGGTGGGGATCGGGTTGGGGGCGGGGTCGGCGCGAGTTTCGGGCGT
TTTTCGTTGTATGGCGGGATTTGTAGTTTTTTAGGGTCGTCGTGGGCGGGG
TCGTAGCGAAGGCGGGGGCGGGAATGTTCGGGCGCGAGTCGTTTGTTATA
ATTTATTTATAGTAATGACGGTTTTTGTAAATTATATATTATTTTTGTTTTC
GTAGTTAGTATTGAGAAGTAAGTTTTTAAGAGTTGATATTTT
[SEQ ID NO: 8]

FIG 1H

TTGTGGAGCGGAGGAGGGGAGGTTTGGGGTCGCGGCGGTGTGCGTTTCGT
TTTGATCGTAGAGTTTTTTTTCGAGGAAAGCGGTTGGTTCGGTTTCGGTT
GGTGATTACGCGGGGTTTTGTTTGTTTGGTGCGTAGGTGAGGGTTTGTTT
TTTCGTTGCGTTTCGGATAGTTTGGAGGTGAGTACGCGTTGGGTTTTGGAT
CGCGAGTAGCGGGAGAAGTACGAGTTGGTGGTCGTGTGTATCGTGTACGT
CGGCGCGCGCGAGGAGGTGGTGATGGTGTTTTTTTCGGTGATCGTGTACG
ACGAGGACGATTCGGCGTTTATTTTTTCGCGGGCGTCGATATCGTTAGCG
TCGTGGTGGAGTTTAAGCGGAAGGAGGTGTTTGTTCGCGCGTGTTGTGGT
TTATTTAGTGTTTGTTTTCGGTTATAGTTCGTTTTTCGGTCGGTTTAGTGTT
CGTGTAGTTATTTAATCGTGTGGTCGATTATTCGCGTTTTTATTTGTTTTTC
GTTTTCGTTTGCGTCGTTTGTTTTAGGGGGAGGGGAAGGGGGAGTTTTGTT
AGTATTTAGTTGGGTTTTGTTTCGGGAGGTAAGGATTAGGACGAGGTTCG
AGGGTTCGCGTTTGGGGTATATTTGTGTCGTTGTAGGCGGGCGCGGCGCG
TTGTTCGGGCGGGGAGTATTTGTCGGGAGGGTATTTTTTTTTATTAGTAGT
TAGTTTTTAACGGGAGGGTTTTTGAGTGATTACGAGTAGAGTCGGGGATT
GGAGAAGGACGGGAAGGCGGATTATTTTCGGCGTCGTTCGTTTCGTTTTTT
TTCGGTTCGCGTTGGTGGAGCGCGATCGTTATTTGTTGG
[SEQ ID NO: 9]
TTAGTAGGTGGCGGTCGCGTTTTATTAGCGCGAGTCGGAGAAGGGCGGGG
CGGGCGGCGTCGGAGGTGATTCGTTTTTTCGTTTTTTTTTAATTTTCGGTTT
TGTTCGTGGTTATTTAAGGGTTTTTTCGTTGGGGGTTAATTGTTGGTGGGA
GGGAGTGTTTTTTCGGTAGATGTTTTTCGTTCGGGTAGCGCGTCGCGTTCG
TTTGTAGCGGTATAAGTATGTTTTAGACGCGAGTTTTCGGGTTTCGTTTTG
TTTTTTTTTTTAGGATAGACGGCGTAGACGGAGGCGAAGGATAAATGAAA
GCGCGAATGGTCGGTTATACGGTTGGGTGGTTATACGGATATTAAATCGA
TCGAGAAACGAATTGTGGTCGGAGATAGATATTGGGTAGATTATAGTACG
CGCGGATAAGTATTTTTTTTCGTTTGAATTTTATTACGGCGTTGGCGGTGT
CGACGTTCGCGGGGAAGGTGGGCGTCGAGTCGTTTTCGTCGTATACGGTT
ATCGGGAAGGGTATTATTATTATTTTTTCGCGCGCGTCGGCGTGTACGGTG
TATACGGTTATTAGTTCGTATTTTTTTCGTTGTTCGCGGTTTAGGGTTTAGC
GCGTGTTTATTTTTAGGTTGTTCGGGGCGTAGCGGAAGGGTAGATTTTTAT
TTGCGTATTAAGTAGATAGGGGTTTCGCGTGATTATTAGTCGGGATCGGG
TTAGTCGTTTTTTTCGGGAAGGGGGTTTTGCGGTTAGAGCGGGGCGTATAT
CGTCGCGGTTTTAGGTTTTTTTTTTTTCGTTTTATAG
[SEQ ID NO: 10]

FIG 1I

ATCGTTTTTTCGTAGGGGTTTTAGGATTTATTTAGATTTCGTTTGTTTTTTT
TTTCGCGGTAGGTTTCGTTGTATCGTGTATTTTTTTCGCGAGAAGTTGATTT
TGCGGAAGGCGTTCGTTATTATCGTCGTTATTTGGGTTTTGGCGTTGTTTA
TTATGTGTTTTTCGGTCGTTACGTTGATCGTTATTCGTGAGGAGTATTATTT
TATGGTGGACGTTCGTAATCGTTTTTATTCGTTTTATTTTTGTTGGGAGGTT
TGGTTCGAGAAGGGTATGCGTAGGGTTTATATTATTGTGTTTTTTTCGTAT
ATTTATTTGGCGTCGTTGGCGTTTATCGTGGTTATGTACGTTCGTATCGCG
CGTAAGTTTTGTTAGGTTTCGGGTTCGGTTTTCGGGGGCGAGGAGGTTGCG
GATTCGCGAGTATCGCGGCGTAGAGCGCGCGTGGTGTATATGTTGGTTAT
GGTGGCGTTGTTTTTTACGTTGTTTTGGTTGTCGTTTTGGGCGTTGTTGTTG
TTTATCGATTACGGGTAGTTTAGCGCGTCGTAGTTGTATTTGGTTATCGTT
TACGTTTTTTTTTTCGCGTATTGGTTGGTTTTTTTTAATAGTAGCGTTAATT
TTATTATTTACGGTTATTTTAACGAGAATTTTCGTCGCGGTTTTTAGGTCGT
TTTTCGCGTTCGTTTTTGTTCGCGTTCGTCGGGGAGTTATAAGGAGGTTTA
TTTCGAGCGGTTCGGCGGGTTTTTGTATAGGCGGGTTTTCGTGGTGGTGCG
GTTTAGCGATTTCGGGTTGTTTTTTGAGTCGGGTTTTAGTAGTGGGGTTTTT
AGGTTCGGTCGTTTTTCGTTGCGGAAT
[SEQflDNO: 11]

ATTTCGTAGCGGGAGGCGGTCGGGTTTGGGGGTTTTATTGTTAGGGTTCG
ATTTAGAGGGTAGTTCGGAGTCGTTGGGTCGTATTATTACGAAGATTCGTT
TGTGTAGAAGTTCGTCGGGTCGTTCGGAGTAGGTTTTTTTGTGGTTTTTCG
ACGGGCGCGGGTAGAGGCGGGCGCGGAAGGCGGTTTGGAAGTCGCGGCG
GAAGTTTTCGTTGAAGTAGTCGTAGATGATGGGGTTGGCGTTGTTGTTGA
AGAAGGTTAGTTAGTGCGCGAAGGGGAAGGCGTAGACGGTGATTAGGTG
TAGTTGCGGCGCGTTGAGTTGTTCGTAGTCGATGAGTAGTAGTAGCGTTTA
GAGCGGTAGTTAGGATAGCGTGAAGAATAGCGTTATTATGATTAGTATGT
GTATTACGCGCGTTTTGCGTCGCGATGTTCGCGGGTTCGTAGTTTTTTCGT
TTTCGGGGGTCGGGTTCGGGGTTTGGTAGAGTTTGCGCGCGATGCGGGCG
TATATGATTACGATGAGCGTTAGCGGCGTTAGGTAGATGTGCGAGAAGAG
TATAGTGGTGTAGATTTTGCGTATGTTTTTTTCGGGTTAGGTTTTTTAGTAG
GAGTAGAGCGGGTAGGAGCGGTTGCGGGCGTTTATTATGAAGTGGTGTTT
TTTACGGGTGACGGTTAGCGTGACGGTCGAGGGATATATGATGAGTAGCG
TTAGGGTTTAGATGACGGCGATGGTGACGAGCGTTTTTCGTAGGGTTAGT
TTTTCGCGGAAAGGGTGTACGATGTAGCGGAATTTGTCGCGGGGAGAGAG
ATAGGCGGGATTTGGGTGGGTTTTAGGGTTTTTGCGAGGGGACGGT
[SEQ ID NO: 12]

FIG 1J

TTTAGTTTCGGAATCGCGGATTGCGTTTAGTGACGGATTTAAATTTATTTT
TTTTTTTGATTTCGTCGTAGGATGACGTTTTAATTTTCGGGTGCGTTTATTG
TTTAAGTGATTCGTGAGACGGAGCGGTTTTTTTTTAGAGTTTCGGAAGACG
AAGTGATTTGTTTTACGTTCGTTTCGTTTAGTTTTATTCGTATACGGGGGA
ATTGCGTAGAGGCGGAAGAGGGAGGTTGTCGAGGGGTTTCGAGGAAGTT
TCGGGTACGGCGCGGGGGACGTAGTCGGTTTAAGAGCGAGTTGGTATTGA
GTAAGTAGCGACGGAGTCGGCGAAAGAAGGTTAACGATCGCGAGCGTAA
TCGAATGTATAATTTTAATTCGGTATTGGACGTTTTGCGCGGTGTTTTGTTT
ATTTTTTTAGACGACGCGAAGTTTATTAAGATCGAGACGTTGCGTTTCGTT
TATAATTATATTTGGGCGTTGATTTAAACGTTGCGTATAGCGGATTATAGT
TTGTACGCGTTGGAGTCGTCGGCGTCGTATTGCGGGGAGTTGGGTAGTTT
AGGCGGTTTTTTCGGGGATTGGGGGTTTTTTTATTTTTTAGTT
[SEQ ID NO: 13]

GATTGGGGAGTAGAGGGATTTTTAGTTTTCGGGGGAATCGTTTGGGTTGTT
TAGTTTTTCGTAGTGCGGCGTCGGCGGTTTTAGCGCGTATAAGTTGTGGTT
CGTTATGCGTAGCGTTTGAGTTAGCGTTTAGATGTAGTTGTGGGCGAAGC
GTAGCGTTTCGATTTTGGTGAGTTTCGCGTCGTTTGGGAAGGTGGGTAGG
ATATCGCGTAGGGCGTTTAGTGTCGAGTTGAGGTTGTGTATTCGATTGCGT
TCGCGGTCGTTGGTTTTTTTTCGTCGATTTCGTCGTTGTTTGTTTAGTGTTA
ATTCGTTTTTAGGTCGGTTGCGTTTTTCGCGTCGTGTTCGGAGTTTTTTCGG
GGTTTTTCGGTAGTTTTTTTTTTTCGTTTTTGCGTAGTTTTTTCGTGTGCGA
GTGGGGTTGGGCGGGGCGGACGTGGGGTAGGTTATTTCGTTTTTCGAGGT
TTTGGGGAAGGATCGTTTCGTTTTACGGGTTATTTGGATAGTGGGCGTATT
CGAGGGTTGAGGCGTTATTTTACGGCGGGGTTAGAGGGAAGGGTAAGTTT
GAGTTCGTTATTGGGCGTAGTTCGCGATTTCGAGGTTAGG
[SEQ ID NO: 14]

TTAGTTTCGGTCGTATTGTATAGCGAGGTCGGTTCGGAGTTCGGATGTTGG
GTTCGGTTTCGTCGAGGTTCGGTTTGGTTGTAAAGTAGAGGGGGGCGAGG
GAAGTCGGGTTAGCGGGTGTCGCGGGTAGTCGGCGTTCGGGACGGGGTGT
GGCGTTTAGAGCGTTGTTGTTTTTCGTAGTTAGGAGGTTGGATGTCGGGTT
TGGGTGTTTTTTAGAAGGAGTCGTATTAGCGACGAGGGAAGAGGAATTGG
TTTTTCGGGTAGTTTTTTTCGTTTTAAATTTTTTTTTTTCGCGGAGGGTGGG
CGGGCGGAGGGAGGAAGCGTAGTCGGGGAACGTGGCGTTCGCGTTTTTTT
CGTTCGGGGGTTGCGGTTGGGTTGAGTGTGTTTTTAAATTTGAGTTTTTCG
TTTTTCGCGGTGGGGTCGGGATTCGCGGTTCGGGCGGGGGCGGGCGCGGT
GATTGGCGGTCGGGTCGGGTTCGTTTTTCGGCGTTGGGTAGCGGGGCGTT
GGGGAGTAGCGCGGCGCGTACGGGTCGGGGCGCGTAGGTTTCGTCGTCGG
TGAGTACGGGTTTTTTTTCGCGTGGTTTCGTCGGGTTCGTTTGGTTTGTTTA
TTTTCGGAGTTATTTTTGTTTTCGTATGGGTTGGCGAAGTTGGGAGGAGCG
AGTTGGAGTTAGAGCGCGCGTCGGGCGCGTTTCGTCGTTGTTTGATTCGGC
GTTCGTAGTTCGGGCGTAGTACGTCGGTCGTAGGAGTACGGATGTTTTTCG
GAGTCGCGGGTTGGTAGGTATCGAAGTGTTTTGTTTTGGGGTTGGCGAGG
GGAGGGTAAATTTGGAATTTTTCGGGTATTTTTTAGTTCG
[SEQ ID NO: 15]

FIG 1K

CGGGTTGGGGGGTGTTCGGGGGATTTTAGATTTGTTTTTTTTTCGTTAGTTT
TAGGGTAGGATATTTCGGTATTTGTTAGTTCGCGGTTTCGGGGGGTATTCG
TGTTTTTGCGGTCGGCGTGTTGCGTTCGAATTGCGGGCGTCGAGTTAGGTA
GCGACGGGGCGCGTTCGGCGCGCGTTTTGGTTTTAGTTCGTTTTTTTTAAT
TTCGTTAGTTTATGCGGGGGTAGAGGTGGTTTCGGAGGTGGGTAGGTTAG
GCGGATTCGGCGAGGTTACGCGAGAGGGAGTTCGTGTTTATCGGCGACGG
GATTTGCGCGTTTCGGTTCGTGCGCGTCGCGTTGTTTTTTAGCGTTTCGTTA
TTTAACGTCGAGGGGCGGATTCGATTCGGTCGTTAATTATCGCGTTCGTTT
TCGTTCGGATCGCGAGTTTCGGTTTTATCGCGAGGGGCGGGGGGTTTAGA
TTTAAAGATATATTTAGTTTAGTCGTAGTTTTCGGGCGGGAGGAACGCGG
GCGTTACGTTTTTCGGTTGCGTTTTTTTTTTCGTTCGTTTATTTTCGCGAG
GAGGAAAAGTTTGGGGCGGGGGAGATTGTTCGGGAAGTTAGTTTTTTTTT
TTTCGTCGTTAGTGCGGTTTTTTTTGGAAGATATTTAAATTCGATATTTAGT
TTTTTGGTTGCGAGAGGTAGTAGCGTTTTGGGCGTTATATTTCGTTTCGGA
CGTCGGTTATTCGCGATATTCGTTGGTTCGGTTTTTTTCGTTTTTTTTTGTTT
TATAGTTAGGTCGAGTTTCGGCGGGATCGAGTTTAGTATTCGGGTTTCGGG
TCGGTTTCGTTGTGTAGTGCGGTCGGAGTTGG
[SEQ ID NO: 16]

TTTTGTATAGGAGTAGTGATTTTAGTATTTATTTAATTTTTTTTCGGCGTCG
AGTTTAGTTGGAGAGGTTAGGGGTGGTAGTGATTGGTAGGAGGTCGGGGC
GGGGGGAATTTTTAAGTTCGGCGTTTGGGGTTGCGGGTTCGATTCGAGAT
TCGTTTTTTTTGTAAGTTTCGAGTCGTTGGTTAGGTTCGTTATTGCGTATTA
GTCGTATTCGCGAGCGTTGGTTTTGTCGGTTTGAGTTAGGGTGGGTAGGGT
CGGGATTTACGGCGGAGGTGGGGTCGGGTCGAGTAGTTTCGGGGGATTTT
CGAAGTTATAGCGTTTTGTTTTTTTGTACGTTTCGCGTTTTCGGTTTTCGAT
TGGTTGTCGGGTTTAGAGTTCGTTTAGAATTGGATCGTTCGTTTGTCGTTC
GGGTTTGGTTTTATTTTTAGAGGGAGTTTAGAATTTGGTCGTAGTTTTTAG
AGATTATTTTTATTTCGTGGTTTGCGTCGAAGTTGGGCGGAGGATAGTGGG
TGGTTAGGTTTTTTCGGGTTAGAATTCGGGATTTTTGTTAGTTATTCGTGTT
AGGATAGATTTAAGTTTTTAAAACGCGGATGGATGTAT
[SEQ ID NO: 17]

GTATATTTATTCGCGTTTTGGGGGTTTGAGTTTGTTTTGGTACGGGTAGTT
GGTAGGGGTTTCGAGTTTTGGTTCGGAAGGGTTTGGTTATTTATTGTTTTT
CGTTTAATTTCGGCGTAGGTTACGGGGTGAGGGTAGTTTTTAAAAATTGC
GATTAGGTTTTAGGTTTTTTTTGGGGGTGGAGTTAGATTCGAGCGATAAGC
GAACGGTTTAATTTTGGGCGGGTTTTAGGTTCGATAGTTAATCGGAGGTC
GGGGGCGCGGAGCGTGTAGGGAGGTAAGGCGTTGTAGTTTCGGGGATTTT
TCGAGGTTGTTCGGTTCGGTTTTATTTTCGTCGTGGGTTTCGGTTTTATTTA
TTTTAGTTTAGGTCGGTAGAGTTAGCGTTCGCGGATGCGGTTGGTGCGTAG
TAGCGGGTTTGGTTAGCGGTTCGGGGTTTGTAGGGAGGGCGGATTTCGGG
TCGGATTCGTAGTTTTAGACGTCGGGTTTGGGGGTTTTTTTCGTTTCGGTTT
TTTGTTAGTTATTATTATTTTTAGTTTTTTTAATTGAGTTCGGCGTCGGGAG
AGGATTAAGTAAGTGTTGAGGTTATTGTTTTTGTGTAAGA
[SEQ ID NO: 18]

FIG 1L

ATCGTTTTTTCGTAGGGGTTTTAGGATTTATTTAGATTTCGTTTGTTTTTTT
TTTCGCGGTAGGTTTCGTTGTATCGTGTATTTTTTTCGCGAGAAGTTGATTT
TGCGGAAGGCGTTCGTTATTATCGTCGTTATTTGGGTTTTGGCGTTGTTTA
TTATGTGTTTTTCGGTCGTTACGTTGATCGTTATTCGTGAGGAGTATTATTT
TATGGTGGACGTTCGTAATCGTTTTTATTCGTTTTATTTTTGTTGGGAGGTT
TGGTTCGAGAAGGGTATGCGTAGGGTTTATATTATTGTGTTTTTTTCGTAT
ATTTATTTGGCGTCGTTGGCGTTTATCGTGGTTATGTACGTTCGTATCGCG
CGTAAGTTTTGTTAGGTTTCGGGTTCGGTTTTCGGGGGCGAGGAGGTTGCG
GATTCGCGAGTATCGCGGCGTAGAGCGCGCGTGGTGTATATGTTGGTTAT
GGTGGCGTTGTTTTTTACGTTGTTTTGGTTGTCGTTTTGGGCGTTGTTGTTG
TTTATCGATTACGGGTAGTTTAGCGCGTCGTAGTTGTATTTGGTTATCGTT
TACGTTTTTTTTTCGCGTATTGGTTGGTTTTTTTTAATAGTAGCGTTAATT
TTATTATTTACGGTTATTTTAACGAGAATTTTCGTCGCGGTTTTTAGGTCGT
TTTTCGCGTTCGTTTTTGTTCGCGTTCGTCGGGGAGTTATAAGGAGGTTTA
TTTCGAGCGGTTCGGCGGGTTTTTGTATAGGCGGGTTTTCGTGGTGGTGCG
GTTTAGCGATTTCGGGTTGTTTTTTGAGTCGGGTTTTAGTAGTGGGGTTTTT
AGGTTCGGTCGTTTTTCGTTGCGGAAT
[SEQ ID NO: 11]

ATTTCGTAGCGGGAGGCGGTCGGGTTTGGGGGTTTTATTGTTAGGGTTCG
ATTTAGAGGGTAGTTCGGAGTCGTTGGGTCGTATTATTACGAAGATTCGTT
TGTGTAGAAGTTCGTCGGGTCGTTCGGAGTAGGTTTTTTGTGGTTTTTCG
ACGGGCGCGGGTAGAGGCGGGCGCGGAAGGCGGTTTGGAAGTCGCGGCG
GAAGTTTTCGTTGAAGTAGTCGTAGATGATGGGGTTGGCGTTGTTGTTGA
AGAAGGTTAGTTAGTGCGCGAAGGGGAAGGCGTAGACGGTGATTAGGTG
TAGTTGCGGCGCGTTGAGTTGTTCGTAGTCGATGAGTAGTAGTAGCGTTTA
GAGCGGTAGTTAGGATAGCGTGAAGAATAGCGTTATTATGATTAGTATGT
GTATTACGCGCGTTTTGCGTCGCGATGTTCGCGGGTTCGTAGTTTTTTCGT
TTTCGGGGGTCGGGTTCGGGGTTTGGTAGAGTTTGCGCGCGATGCGGGCG
TATATGATTACGATGAGCGTTAGCGGCGTTAGGTAGATGTGCGAGAAGAG
TATAGTGGTGTAGATTTTGCGTATGTTTTTTTCGGGTTAGGTTTTTTAGTAG
GAGTAGAGCGGGTAGGAGCGGTTGCGGGCGTTTATTATGAAGTGGTGTTT
TTTACGGGTGACGGTTAGCGTGACGGTCGAGGGATATATGATGAGTAGCG
TTAGGGTTTAGATGACGGCGATGGTGACGAGCGTTTTTCGTAGGGTTAGT
TTTTCGCGGAAAGGGTGTACGATGTAGCGGAATTTGTCGCGGGGAGAGAG
ATAGGCGGGATTTGGGTGGGTTTTAGGGTTTTTGCGAGGGGACGGT
[SEQ ID NO: 12]

FIG 1M

TGGTTACGAAGAATCGGTTGGTTACGTCGAAGATGTTTATTACGTTTCGTT
TTACGGGCGAGAGTTTTAGTAGGTTTGGGGGCGGGGCGTAGGTTATTGCG
GGGTAGGTGATTTTTGGTTTATTTCGTTTTTCGGTTTGTTCGTTTTCGGGGA
TTTTATTTTTGGGGTGGGGTTGGGGATAAAGGGTTAGGGTTTTCGGCGTAG
TCGTTTTTAAGGGTTTTTAGAGTTTAAGTTGTTTTTTAGGGTTTTCGGAGTT
TAAGTTTGCGTTAGTTTAGATTAGTTTGTTTGTGTAGGGGATTTTCGGCGG
TCGTATTTAGTTTCGGATTTTTAGACGCGAGTTCGATTTTAGCGGTTTTTTA
GTTTGGGTTAGGTCGGGGCGCGTGTTTCGGGTTTTTTGTGGTTGTATCGCG
CGTTTTGTGTTTACGGGCGAAGGCGTTGGAATTCGGCGTTCGGAGTTCGA
GTTTTTGAAGGCGGGAGGCGGCGTTCGATTTTAGGGGTTGCGTTGGGTTG
TCGGAGTTAAGAGTGTTTGCGTTTTTAGTTTCGCGTTAGAAGGGATCGGA
GTTCGAGTTCGTTTCGGTTTTCGGGGTTTTCGAGTAGGTGTTCGTCGAGGG
TTTTAGAGTGTGATTGAGCGGGTTGGTTCGGCGGTCGTTGTTTTTCGTTTT
CGTTTTTTCGCGTTTGGTCGCGTTATTTATTGTCGCGGGTGTTCGCGTGCGC
GTCGTCGATGCGGTCGTCGGGGAGCGTTTGGAGGTGGAAGTCGATGTTTA
CGTTGTAGTAGAGTCGTCGTAGTCGTTTGATGTTTAGTAGGTAGTCGTCGG
CGTCGTTTTGGACGGTCGTTTTTTTGGGTTGCGTTGTTATCGGTAGGCGCG
TTAACGAGAGCGTTATTAGGTTTTTTTAGCGGCGTTTTAGTTCGGTTTTTA
GCGTGTCGTTGGGTGTAGTGGGTGCGGCGGCGTTTTTTCGGTTCGTTTAGG
GCGTTAGTAAGGTTAGTAGGATCGTCGGGAGTAGCGTTATCGCGGTCGTT
TCGGGTTTCGATATTTCGGTTCGAGGGTCGTGCGTCGGTTAGGCGGTTAGT
GCGTTCGGGAAGTTGGGGGGTAGAGTTGCGTTTGTGGCGTTTCGCGGGAG
CGTACGGTCGATTTCGGGTAGGAGTGCGTAATCGAGGAGGTGCGGGAGGT
AAGCGACGGGGTTTTCGGGCGTCGGGTTTTATTTCGGTTGTATGGAGCGG
CGAGTCGGGCGGAAAGCGCGCGGTTGGAGTTGGGATTTTGAGGAGTAGT
GCGCGTTTTTTTGAGCGTTAGGTTCGTTCGAGGTCGAGTCGTTATATATAT
AGTTCGGCGTTTTTTTTTATTCGTTCGTTTTCGCGGGGGGTCGTTCGCGTTT
TTTTGGGCGTTCGGGGCGTTGTGGCGTTCGCGGTTGGTCGTAGGTCGTTTG
TTAATTAGGGTCGGGGGAAGGGAGGAGGTTGGGGATTAGCGTCGCGAGT
GTTATTTGGAGGGATTTCGGTTTTTATTTTTGGTTTCGTTCGGTTTACGGAT
TTGTTCGTTTCGTTTTTTGGCGGTTTTTATATTTTTGTTTTTTAGTTAGTTTT
GTTTTTTGTATTTTGTTTTTGTTT
[SEQ ID NO: 20]

FIG 1N

AGGGTGAAGTTTGAGAGTTTAAATGGTTAATTTTATAGGGTTGAACGTTTT
AGAAGTCGTAGGTTCGTTGGGGTTGATTTTGGTAGTTGTCGTGGAGGTGG
GGGTATTGTTGGGTAACGGCGCGTTGTTGGTCGTGGTGTTGCGTACGTCG
GGATTGCGCGACGCGTTTTATTTGGCGTATTTGTGCGTCGTGGATTTGTTG
GCGGTCGTTTTTATTATGTCGTTGGGTTTGTTGGTCGTATCGTCGTTCGGGT
TGGGTCGCGTGCGTTTGGGTTTCGCGTTATGTCGCGTCGTTCGTTTTTTTT
CGTCGTTTTGTTGTCGGTTTGTACGTTCGGGGTGGTCGTATTTGGTTTGGT
ACGTTATCGTTTTATCGTGTATTCGTTGCGGTTAGGTTCGCGGTCGTCGTTT
GTGTTCGTGTTTATCGTCGTGTGGGTCGCGGCGGGATTGTTGGGCGCGTTT
TTTTTGTTCGGTACGTCGTTCGTATCGTTTTTTGTTTTTGTTCGTTGTTCGGT
TTTGGTTGGGGGTTTCGGGTTTTTTCGGTCGTTTTGGGTTTTGTTGGTTTTC
GCGTTGTTCGTTTTTTTGTTGTTCGGCGTTTACGGCGGTATTTTCGTGGTGG
CGCGTCGCGTTGTTTTGAGGTTTTTACGGTCGGCGCGCGGGTTTCGATTTT
ATTCGGATTTTTTGGATAGTCGTTTTTTTATTTTGTCGTCGTTTCGGTTTCG
TTTGTTCGGGGGTAAGGCGGTTTTGGTTTTAGCGTTGGTCGTGGGTTAATT
TGTAGTTTGTTGGTTGTTTTATGGTTGCGCGTGTTTGGCGTTCGTAGCGCG
GGTCGCGGAAGTCGAAGCGGTTGTTATTTGGGTCGTTTATTCGGTTTTCGC
GGTTTATTTTTTTTTGTACGGGTTGTTGTAGCGTTTCGTGCGTTTGGTATTG
GGTCGTTTTTTTCGTCGTGTATTGTTTGGATTTGTGCGGGTTTGTATTTCGT
AAGTTTGGTATTCGCGGGTATTTTTGTAATGTTTTTAGAGATTTTTAGAGG
GTTTTGTCGTAGGTTTTTTTGAGGTTTTAGAATAGATTTTCGAGTTGGTAG
GAGGGCGGAGTTTCGTATATT
[SEQ ID NO:21]

GGTATGCGGGGTTTCGTTTTTTTGTTAATTCGGGGGTTTGTTTTGGAGTTTT
AGAAGGGTTTACGGTAGGGTTTTTTGGGGGTTTTTGGAGGTATTGTAAGA
GTGTTCGCGGGTGTTAGGTTTGCGGAGTGTAGGTTCGTATAGGTTTAGGTA
GTGTACGGCGAGAGAGGCGGTTTAGTGTTAAGCGTACGGGGCGTTGTAGT
AGTTCGTATAGGAAGGGGTGAGTCGCGAAGGTCGAGTAGGCGATTTAGGT
GATAGTCGTTTCGGTTTTCGCGGTTCGCGTTGCGGGCGTTAGGTACGCGTA
GTTATAAGGTAGTTAGTAGGTTGTAAATTGGTTTACGGTTAGCGTTGGGGT
TAGGGTCGTTTTGTTTTCGGGTAGGCGAGGTCGGAGCGGCGGTAAGATGG
AAAGGCGGTTATTTAGAGAGTTCGAGTGGAGTCGGGATTCGCGCGTCGGT
CGTGGGGGTTTTAGGGTAGCGCGACGCGTTATTACGAAGATGTCGTCGTA
GGCGTCGAGTAGTAGGAGGGCGGGTAGCGCGAAGGTTAGTAGGGTTTAG
AGCGGTCGGAAGGGTTCGAGGTTTTTAGTTAGGATCGAGTAGCGAGTAGG
AGTAGGGGGCGGTGCGGGCGGCGTGTCGAGTAGGGAGAGCGCGTTTAGT
AGTTTCGTCGCGGTTTATACGGCGGTGAGTACGAGTATAGGCGGCGGTCG
CGAGTTTGGTCGTAGCGGGTGTACGATGAGGCGGTAGCGTGTTAGGTTAA
GTGCGGTTATTTCGAGCGTGTAGGTCGGTAGTAGAGCGGCGGAGAGGAA
GCGAGCGGCGCGGTATGGCGCGGGGTTTAGGCGTACGCGGTTTAGTTCGG
GCGGCGGTGCGGTTAGTAGGTTTAGCGGTATGATGGAGGCGGTCGTTAGT
AGGTTTACGACGTATAGGTGCGTTAGGTAGAGCGCGTCGCGTAGTTTCGG
CGTGCGTAGTATTACGATTAGTAGCGCGTCGTTGTTTAGTAGTGTTTTTAT
TTTTACGATAGTTGTTAGGATTAATTTTAACGAGTTTGCGATTTTTGAGGC
GTTTAGTTTTGTGGAGTTGGTTATTTGGGTTTTTAGGTTTTATTTT
[SEQ ID NO: 22]

FIG 1O

GGTGTCGGTGTTGGTGTTGTTTATGGTCGCGTTGTATTAGGTGTTTAATAA
GTGGATATTGGGTTAGGTAATTTGCGATTTGTTTATCGTTTTCGACGTGTT
GTGTTGTATTTTATTTATTTTGTATTTGTGCGTTATCGCGTTGGATAGGTAT
TGGGTTATTACGGATTTTATCGATTACGTGAATAAGAGGACGTTTCGGCG
CGTCGTTGCGTTTATTTCGTTTATTTGGTTTATTGGTTTTTTTATTTTTATTT
CGTTTATGTTGGGTTGGCGTATTTCGGAAGATCGTTCGGATTTCGACGTAT
GTATTATTAGTAAGGATTATGGTTATATTATTTATTTTATTTTTGGAGTTTT
TTATATTTCGTTGTTGTTTATGTTGGTTTTTTATGGGCGTATATTTCGAGTT
GCGCGTTTTCGTATTCGTAAGACGGTTAAAAAGGTGGAGAAGATCGGAGC
GGATATTCGTTATGGAGTATTTTTCGTTTCGTAGTTTAAGAAGAGTGTGAA
TGGAGAGTCGGGGAGTAGGAATTGGAGGTTGGGCGTGGAGAGTAAGGTT
GGGGGTGTTTTGTGCGTTAATGGCGCGGTGAGGTAAGG
[SEQ ID NO: 23]

TTTTGTTTTATCGCGTTATTGGCGTATAGAGTATTTTTAGTTTTGTTTTTTA
CGTTTAGTTTTTAGTTTTTGTTTTTCGATTTTTTATTTATATTTTTTTTGGGT
TGCGGGGCGGGAGATGTTTTATGGCGGGTGTTCGTTTCGGTTTTTTTTATT
TTTTTGATCGTTTTGCGGATGCGGAAGCGCGTAGTTCGGAATATGCGTTTA
TAGAGAATTAGTATGAGTAGTAGCGGGATGTAGAAAGTTTTAAAGGTGGA
ATAGATAGTGTAGTTATGATTTTTGTTAATGGTGTATGCGTCGGGGTTCGA
GCGGTTTTTCGGGGTGCGTTAGTTTAGTATGGGCGGGATAGAGATGAGGA
AGTTAATAAGTTAAGTGAGCGAGATGAGCGTAGCGGCGCGTCGGGGCGTT
TTTTTGTTTACGTAGTCGATGGGGTTCGTGATGGTTTAGTATTTGTTTAGC
GCGATGGCGTATAGGTGTAAGATGGATGAGGTGTAGTATAGTACGTCGAG
GGCGATGAATAGGTCGTAGGTTATTTGGTTTAGTGTTTATTTGTTGAGTAT
TTGATATAGCGCGGTTATGGGTAGTATTAATATCGATATT
[SEQ ID NO: 24]

GGGATGATAAGGGAGAAAAATTTTTTTACGGTTTCGTTTGGTTCGCGGCG
TTTGTTTGTTTGCGCGGGGTTAAAGTTCGGCGTCGTTTACGCGCGGTTCGG
GTGGGAATTCGTAGACGTGGGGCGAGTAGGGTCGTTGGTTGTGGCGGGCG
AGCGTCGGGGCGTTACGTTCGAGGTCGCGGGGTCGGGGTTGTAGGTATAG
TTCGAGCGTTTTTCGCGGGGTTTGGTTTTTGTCGTTTTTCGTTTCGTCGAAT
CGGTATCGTCGTCGTCGGAGTCGTAGCGAGTTTTTAGAGTTTGGTTGTTGG
CGGTCGGGAGCGTCGGGACGGGGCGCGAAGTCGGAGGTTTCGGGACGTG
GATATAGGTAAAGGTCGGCGGGTCGGAGTCGGGCGGGGCGCGGCGGCGG
CGTTTTTCGGAGGGATTTGGTTTCGGTCGGGTTTTATTTAGTCGCGGTGGT
TCGGGTTTTTACGTTGGTTTAGGCGGGGACGTGTTAAGGGGTTGGGTTAG
GGTTGTCGTTGGTTTGGTCGTTTTTCGTTCGGCGGGTTTTAGGTGACGCGG
TCGCGGTTTAATTTTCGTATTTGAGGTTTTCGGAGCGGTTTCGGGGCGCGT
TTATTTGGAGGTTGGAATTATATAGGGTCGAAAAAGTTGAGTTTTGGAGG
CGAGGCGTTGTAGGTGTGGCGGAGGAGGTCGGGGAAGGTGGGGTGGGTG
TTAGGGGTTTAGTATTGAATTTTTTTTAGGTTTGAGGTGGGGAATTGCGTT
TTGTTTAATTTCGGAGTTTGTGGGGATTATATAGTTTTTTTTACGGTCGATT
TTTTTTGTACGGTTTTATTTTTTTTTGTTTAGTTTATTTTAGT
[SEQ ID NO: 25]

FIG 1P

ATTGAAATGGGTTAGATAAAGGAAAGTGGAATCGTGTAGAGGGAATCGG
TCGTGGAAGGGGTTGTGTGGTTTTTATAAGTTTCGAAATTAAATAAGACG
TAGTTTTTTATTTTAGATTTGGAGAGGGTTTAGTATTGGATTTTTGGTATTT
ATTTTATTTTTTTCGGTTTTTTTCGTTATATTTATAGCGTTTCGTTTTTAGGA
TTTAGTTTTTTCGATTTTGTGTAATTTTAATTTTTAGGTGGGCGCGTTTCGA
GGTCGTTTCGAGAGTTTTAGGTGCGAAAGTTAAGTCGCGGTCGCGTTATTT
GAGGTTCGTCGGGCGAGAGGCGGTTAGGTTAGCGGTAATTTTAGTTTAGT
TTTTTGGTACGTTTTCGTTTGGGTTAACGTGGGGGTTCGGGTTATCGCGGT
TGGGTAGGGTTCGGTCGAGGTTAGGTTTTTTCGAGAGGCGTCGTCGTCGC
GTTTCGTTCGATTTCGATTCGTCGGTTTTTATTTGTATTTACGTTTCGGAGT
TTTCGGTTTCGCGTTTCGTTTCGGCGTTTTCGGTCGTTAGTAGTTAGGTTTT
GAGGATTCGTTGCGGTTTCGGCGGCGGCGATGTCGGTTCGGCGAGACGGG
AAGCGATAGGAGTTAAATTTCGCGGAAAGCGTTCGAGTTGTGTTTGTAGT
TTCGATTTCGCGGTTTCGGACGTGGCGTTTCGGCGTTCGTTCGTTATAGTT
AGCGGTTTTGTTCGTTTTACGTTTGCGGGTTTTTATTCGAGTCGCGCGTGG
GCGGCGTCGGGTTTTGATTTCGCGTAGGTAGATAAGCGTCGCGGGTTAGA
CGGAATCGTGGAAAGTTTTTTTTTTTGTTATTTT
[SEQ ID NO: 26]

TGAGGTGTGGGGATTATTTATTTCGGTGGGTTTTTTTATTTTTAGGTCGGTT
TTTTTATTACGCGTGGGTGTGGGGGTATTGTTTTCGTTGCGCGTAGGAATA
GCGGGGAGAGTTAGGAGCGGAGCGGTTTCGGGATGTTAGATTGAGTAGT
GGGTTCGTTTGCGGTTATTTTTTAGGGAATAAGTTTTTTTCGCGGAGATT
TTGTTTTTTTTAAAAGTTTTTTTGGGTTTAGTTTAGGGCGATAGGACGATTT
TTTTTGGGAAGGGAGAGTTTGTTAGTTTTTTTTTTATTCGTTAGGCGGTGT
AGTTTTTTTTTTCGTTCGGGGCGCGCGTATTTTAGCGTCGCGGGTTTAGCG
TTTAGTAGTCGCGTTTTAGGTCGGGTTTCGGGTTTCGGGAGTTCGTAGGCG
CGCGTTCGGTCGGGCGTGTCGGGAGCGCGCGGCGGTCGGGGGCGGAGCG
TAGTTAGGGTTGCGCGGCGCGTTTCGGTTTTCGTTCGTTTTTAGTCGGGTT
TTTTAGCGGTCGGCGGGACGGTTTTCGGTTGTAGTTTGTTCGTTCGTTTCG
CGCGGGGGTCGAGTCGCGAAGCGCGTTTGCGATTCGGCGTTCGGGCGCGT
TGGAGAGGACGCGAGGAGTTATGAGGCGTTAGTTTGCGAAGGTGGCGGC
GTTGTTGTTCGGGTTGTTTTTGGAGGTAGGGGTCGGGGATCGGGTGTTGTC
GGAGGCGCGGCGTTTATTATGTTGGCGGTTGGGGGCGCGTAGTTTCGAGG
CGTTTTAGAGGATTTTGTTTGGGAGCGTAGACGGTGGAGCGACGGGGAGT
TATAGTTTTGCGCGTTTTTCGGAGTTGGGAGGTGCGGGATTTTGGTGACGG
GGAGGTTTTCGTTTCGGTTCGCGTTTTTCGTCGTTTTTTCGGTTTTCGTATT
TCGTTTTTATTTTGCGGGTGAGCGCGTTTTTCGCGTCGATCGTTTTCGTTAG
TTCGGGGTGATTTTGTGTATCGTTCGTTTTTTTTTTCGTCGTAGAGGGTC
GAGGATCGGATGGATTCGGGGTTGGGCGGGGGTGGTTTTCGGGCGCGGCG
TAGGCGCGGAGAGTTCGGGGCGTCGGGTAGTTTGGGGTTAGGAAAGGAT
GGGTGTCGAGTCGGGGTGAGGGGAGCGGGCGGAGGGGATTGTGGGGAAG
TGTCGCGGGAGTGTCGGGAGTTGTGGAGGTGAGTAGCGGGAGGAGGCGT
TTTCGCGTGTGAAAATGAAGTGTAGTTTTTAGGTGCGGGGAGGAAATTTT
GCGGAGAGTTTGGTTGGGTGGGGGTGCGGAGTCGAAGTCGGCGGGGAAT
TTGTTGAGCGGTTTTCGGGTGCGAGCGTTCGTGATCGT
[SEQ ID NO: 27]

FIG 1Q

GCGGTTACGGGCGTTCGTATTCGGAAGTCGTTTAATAAGTTTTTCGTCGGT
TTCGGTTTCGTATTTTATTTAGTTAGGTTTTTCGTAGAATTTTTTTTCGTA
TTTAAAGGTTGTATTTTATTTTATACGCGGGAACGTTTTTTTTCGTTGTTT
ATTTTATAATTTTCGGTATTTTCGCGATATTTTTTTATAGTTTTTTTCGTTC
GTTTTTTTTATTTCGGTTCGGTATTTATTTTTTTTTAATTTTAAATTGTTCGG
CGTTTCGGGTTTTTCGCGTTTGCGTCGCGTTCGAGGATTATTTTCGTTTAAT
TTCGGGTTTATTCGATTTTCGGTTTTTTGCGGCGGGGAGAGGGGGCGGAC
GGTGTATAAAGGTTATTTCGAGTTAACGGAGGCGGTCGGCGCGGGAAACG
CGTTTATTCGTAGGGTGGGGGCGGGGTGCGAAAATCGAAGGAACGACGG
AAGGCGCGGATCGGGGCGGGAGTTTTTTCGTTATTAGGGTTTCGTATTTTT
TAGTTTCGGGAGGCGCGTAGGGTTGTGGTTTTTCGTCGTTTTATCGTTTGC
GTTTTTAGGTAAGGTTTTTTGGGGCGTTTCGGAATTGCGCGTTTTTAGTCG
TTAGTATGGTGGGCGTCGCGTTTTCGGTAGTATTCGGTTTTCGGTTTTTATT
TTTAAGAGTAGTTCGAGTAGTAGCGTCGTTATTTTCGTAGGTTGGCGTTTT
ATGGTTTTTCGCGTTTTTTTTAGCGCGTTCGGACGTCGGGTCGTAGGCGCG
TTTCGCGATTCGGTTTTCGCGCGGGGCGGGCGGGTAGATTGTAGTCGGGA
GTCGTTTCGTCGATCGTTGGGGGGTTCGGTTGGGAGCGGGCGGGAGTCGG
GGCGCGTCGCGTAGTTTTGGTTGCGTTTCGTTTTCGGTCGTCGCGCGTTTT
CGATACGTTCGGTCGGGCGCGCGTTTGCGGGTTTTCGGAATTCGAGGTTC
GGTTTGGGGCGCGGTTGTTGGGCGTTAGGTTCGCGACGTTGAGGTGCGCG
CGTTTCGGGCGGGAGGAGGGGTTGTATCGTTTGGCGAATGGGAGGGGGAT
TGGTAGGTTTTTTTTTTTTAAGGGAGGTCGTTTTGTCGTTTTAGATTAAATT
TAGGAAGGTTTTTAAAAGAAGTAGAGTTTTCGCGGGGGGAAGTTTGTTTT
TTGAGAGGTGGTCGTAGACGAATTTATTGTTTAGTTTGGTATTTCGAAGTC
GTTTCGTTTTTGGTTTTTTTCGTTGTTTTTGCGCGTAGCGGGGGTAGTGTTT
TTATATTTACGCGTGATGGGAAGGTCGGTTTGGGGGTGGGAAGGTTTATC
GAAATAGATGGTTTTTATATTTTA
[SEQ ID NO: 28]

FIG 1R

AATTTAGAAATAAATAAATATATATGTATACGTATATAAATATATTTTAA
ATTAAAAAATATTTTTAGATAGTGGTATGTATTATATTTAGAAATTAATAA
CGAAGTAAATTATGGGATGTTATTTACGTTTGTTTTAAAGGTATCGAATTT
ATAAATTATTTTAGGTGCGGAGTAGGATAGGTTGAAAATAGGAATGATAT
GAATTCGCGCGGAATAGTTGTCGGCGCGGTGTTTAGGGCGGTATTTCGTT
CGGTTTCGGTTTTTTTAGTTTTGGGTTCGATTTTTATTACGTTTTTGTTTCG
ACGCGAACGCGGAGTTCGAGCGCGCGTTACGTCGTGTGGGGTCGAAGAG
GTTGTTATTTAGAGGCGGAGTGCGGGTTCGCGAGGGTTTTTATTCGATTTT
CGTTTTCGTTAGTATTTACGGATTCGCGTTTTCGTCGCGCGTCGATTCGGG
AGTAGTATCGTTTTCGGTATAGGAGTTTTACGCGTTTTTTATTTAATAGGA
AGTTGGGTGGAAGTAGCGCGGATTTACGGTATATCGAACGTATTTTAATA
GAATTCGACGTAGATACGCGTTTTTAATCGGCGGAGATATTGGTAGGGTT
AGAAACGCGCGTAGCGGGGGCGGGAGGTCGGTAAGTTTTTCGTTTTTGTT
CGAGATTTCGTTTCGGTTCGGTTTCGTTTTTTTTTTGTTTTTTTTTTTGTA
CGTACGGGTTTCGTTTTTCGCGCGACGTTTTTTGTTGATTCGGAAACGGAT
TTTTCGGAGTCGAGGTTCGTTCGGGTGAGTGTTTTTCGTTTTTTGTGGTTAA
ATTTAGTTACGTAGTTTTTTTTTTGCGGCGTTTTTTATATTCGGGGTTTGTT
GGTTTTCGCGGATGTTATAGGTTCGGTAATCGTTTTTTTGTCGGCGGGGAG
TTTCGCGACGTTCGGAAATGTTTCGAAGTTTGTCGTTTAGTTGTTAGATTT
GCGTTTGTGTTCGGTTTCGTTATTGAGGTCGTTTTTGTTCGGTTTTTTTATT
TTAGTTTTTTTTATCGTTCGTTTATTTTATCGCGCGCGGTTTTAGGTTTCGA
TTCGGTATGTGGTTTGTTTTTTATCGTTTT
[SEQ ID NO: 29]

GGGACGATGGAAGATAAGTTATATGTCGAATCGGGATTTGAGGTCGCGCG
CGATAGGATGGGCGGACGGTGAAGAGAATTAGGGTGGAAGGGTCGGATA
GGGGCGATTTTAGTGACGGAATCGGATATAGACGTAGATTTGGTAGTTGG
GCGATAGGTTTCGGAGTATTTTCGGGCGTCGCGGGATTTTTCGTCGATAGG
AGGGCGGTTGTCGAGTTTGTGATATTCGCGGAGATTAGTAGATTTCGGGT
GTGGAGGACGTCGTAGGAAGGGAATTGCGTGGTTGGGTTTGGTTATAAAA
AGCGGAGGGTATTTATTCGAGCGGATTTCGGTTTCGGAGAATTCGTTTTCG
GGTTAATAAAAAACGTCGCGCGAGGGGCGGGGTTCGTACGTGTAGGGAG
GGGAGGTAGAGAAAAAGGCGGGGTCGGGTCGGGGCGGGGTTTCGGGTAG
GGGCGGGGAGTTTATCGATTTTTCGTTTTCGTTGCGCGCGTTTTTGGTTTTG
TTAGTGTTTTCGTCGGTTGAAAGCGCGTGTTTGCGTCGGGTTTTGTTGGAG
TGCGTTCGGTGTGTCGTGGGTTCGCGTTGTTTTTATTTAATTTTTTGTTAGG
TAAGAGGCGCGTGAGGTTTTTGTGTCGGGGGCGGTGTTGTTTTCGAGTCG
GCGCGCGGCGGGGACGCGAGTTCGTAGGTGTTGGCGGGAGCGAGAGTCG
GGTGGGGATTTTCGCGAGTTCGTATTTCGTTTTTGGGTAGTAGTTTTTTCG
GTTTTATACGGCGTGACGCGCGTTCGGGTTTCGCGTTCGCGTCGAGGTAG
AGGCGTAGTAGGGGTCGGGTTTAGGGTTGGAGGGGTCGGGATCGGGCGG
GGTGTCGTTTTGGATATCGCGTCGGTAGTTGTTTCGCGCGGGTTTATGTTA
TTTTTATTTTTAATTTGTTTTGTTTCGTATTTGAGATGATTTATAAATTCGG
TATTTTTGGGATAGGCGTGGATGATATTTTATAATTTATTTCGTTATTAATT
TTTAAATGTAATATATATTATTATTTAAAAGTATTTTTTAATTTGAAATAT
ATTTGTATACGTATATATGTATATTTATTTATTTTTGAATT
[SEQ ED NO: 30]

FIG 1S

TGCGCGTTGTTGCGTTGAGGTCGAATGAAGCGTAGTACGGTGCGGGTAGT
TCGAGGTTTCGAGGTTGGGTTTTGTTTGTTTGGGATTGCGTCGTGTTTAGT
TTCGGTTTTTTTTTGTGGGTAAGGATGGTTGAGTTTAGTTTTACGGTAGC
GGTTTTTTGTGTTATTAGTAGTTTTTTTTTTGCGTTTTTCGTTTTTTTTTTT
AGATTGGATTTTTTTTTTTTTTCGCGTTTTTTTTTTCGTATTTTTATTCGTT
GGTTTTTTTTTTAGTTGTTTTTTTTTTAGGTTTTTTTTGGTTGCGCGCGTTTT
TTTTTTCGTTTTTTTTTTTTTCGTAGTTTCGTCGTTTTGGTGTTTTTTTGTTCG
GTTCGGTCGGCGTTCGTTTTCGGTTTCGGTTTCGTTAGTTCGGGTTTTCGCG
TTCGGAGTAGTTTAGTTTTGTAGTGGTTCGGGATTCGATGTTATGAGAGGG
AAGCGAGTCGGGCGTTTAGATTTTTAGGAGGCGTCGGATGCGCGGCGGGT
TTTGGGATCGGGTTTTTTTTTCGGTTCGTTTTGTTTTCGGGTGATTATTTGG
TTTCGTTTATAGTTTTGTTTTTTTCGGAGGAGTTATCGGTGTCGCGTGCGTG
TGGAGTATTTGTAGATATGATTGCGTGGAGGAGATTTTAGTCGTTGTTTTT
GTTTTTCGGGTTGTTGGTGTTGTGCGCGAGGTTTTTTATTGTAGCGAAGGG
TAAGACGGATTTGTTTTTGGTCGGGGAGGCGGTAGAGTTTTCGGAGGTTT
CGTGTGCGGACGCGAGTGTGCGTTTTGGGGATCGTAGGGTACGGAGTGGT
CGTTTTTGTTCGGCGTTGTTTTATCGTCGAAGTTCGGGGAACGCGATGTAC
GGGAGGGAGTTTTTATCGCGTTTTTTTTAGTTTTTTTGGGTTTTCGTTTTAT
TTCGTTATTTTTTTTTTTTTTTTTTGGGTTTATAGGAGAGATTTTTTTTTTTCG
GTAGTATAGGGTGTTAAGGAGAAAGGAATTTAATACGAGTTGGGTTGGAA
TTGTGTTTCGTCGGGGCGGTGTTGTTTTTTTCGAGACGTGGATTTTACGGG
TCGGGGTGGTTGAGGGGTAGTTTTTAGGATTTTTTTTTCGGATTCGACGCG
TTTGGGAAAGCGTTTCGGGTGAAGTCGGTTTGGAAAGTTCGGGTTTTTTAC
GGGGGTTTTGGTATTAATAGGTAAAGGTTTTCGTCGGTTCGGTTTTTTCGT
ATTTATATATTTTATTTTTTTTTTTTTTTTTTTTTTTTTAACGTTTTTAGTCGG
CGAGGAGTAGTTGTTTTTAGAAGGTCGTTTTCGTTTTTTTTTTTTTCGGATT
TCGTTTTTT
[SEQ ID NO:31]

FIG 1T

AAGGAGCGAAGTTCGGGGGAGAGGAAAGCGGGGGCGATTTTTTAGAGGT
AGTTATTTTTCGTCGGTTGAGGACGTTGGAGAGGGAAGGAGGAGAGGAG
GAATGGGGTGTATGGGTGCGAGGAGGTCGGGTCGGCGGAGATTTTTGTTT
ATTGGTATTAAAATTTTCGTAGAGAGTTCGAATTTTTTAGGTCGGTTTTAT
TCGGGACGTTTTTTTAGGCGCGTCGGGTTCGGGGAGAAAGTTTTGGGAAT
TGTTTTTTAGTTATTTCGATTCGTGGAGTTTACGTTTCGGAGGAGGTAATA
TCGTTTCGGCGGAGTATAGTTTTAGTTTAATTCGTATTGGGTTTTTTTTTT
TTGATATTTTGTATTGTCGAGAAAAAGAGATTTTTTTTGTGAGTTTAAGAG
AGGGGGAAGGAATGGCGGGGTGGGGCGGGGGTTTAGGAGGGTTGGGGAG
AGCGCGATGGAAGTTTTTTTTCGTGTATCGCGTTTTTCGAGTTTCGGCGAT
GGAGTAGCGTCGGGTAGAGGCGGTTATTTCGTATTTTGCGGTTTTTAAAAC
GTATATTCGCGTTCGTATACGGGGTTTTCGAGGGTTTTATCGTTTTTTCGGT
TAGGAGTAAGTTCGTTTTATTTTTCGTTGTAGTGAGGAGTTTCGCGTATAG
TATTAGTAGTTCGAGAAGTAGGAGTAGCGATTGGAATTTTTTTACGTAGT
TATGTTTGTAGATATTTTATACGTACGCGATATCGATGGTTTTTTCGAGGA
AGGTAGGGTTATGAGCGGAGTTAAATAATTATTCGAGGGTAAGGCGAGTC
GGAGAGAGAGTTCGGTTTTAAGATTCGTCGCGTATTCGACGTTTTTTGAAG
GTTTGGGCGTTCGGTTCGTTTTTTTTTTATAGTATCGGGTTTCGAGTTATTG
TAGGGTTGAGTTGTTTCGAGCGCGGAGATTCGGGTTGGCGGGGTCGGGGT
CGGGGACGAGCGTCGGTCGAGTCGGGTAGGAAGGTATTAAGGCGGCGAG
GTTGCGGGAGGGGGAGAAGCGGGGAGAGGAGCGCGCGTAGTTAGGAGA
GATTTGGAGAGGAGGTAGTTGGAGAGAGAGTTAGCGAGTGGGAGATGCG
GGGAGGGGGGCGCGGGGGGGAGGAGAGATTTAGTTTAGAGAGAAAAGG
CGGAGAGCGTAGAAGAAGGGTTGTTAGTGGTATAAGGAGTCGTTGTCGTG
GAGGTTGGATTTAATTATTTTTATTTATAGAGAGGGGATCGAGGTTGGGT
ACGGCGTAGTTTTAGATAGATAGAGTTTAGTTTCGGGGTTTCGGGTTGTTC
GTATCGTGTTGCGTTTTATTCGGTTTTAGCGTAGTAGCGCGTA
[SEQ ID NO: 32]

GATTTTTTGGGTTAGGATATGTGAGAGTTGCGTAGGTTTGGGTTCGGCGTG
GCGGAGGTGCGCGAGAGCGGTTAGAAGAGGGCGTTAGAGAGTTAGGCGC
GGTTCGCGGAGGAGTTCGCGTCGGTTTTTATATTTAGTTTCGCGTCGCGCG
GATTTATCGAGTTCGCGTTTAGACGTTTTAGTTTTATCGAGAGGTCGTTCG
GGTCGTGTTTTTTTTTTTTTTTAGGTGTAGGTAGAGTTTTCGAGTTATGGTT
AGTTTTTTCGGTAGTTTCGAAGTTATTGGTAAGTTTCGAGGTAGGGATGGT
CGGTTTAGGAGGGAGGAGGACGACGTTTTTTTCGAAGAGAAGAGGTTGG
GGTTGTAGTTGGAGGGGGGAAGCGTATAGTTCGAGGATTGCGAGAACGG
GGAGGACGCGTCGCGGTTAGGTAGGGAGGAGATCGGTATTTAGATAGGT
GGCGATCGTAGAGGAGTAAGTGACGCGGGCGTTGGGGTTCGGGGGTGTC
GGGGGCGTCGGTAGGGGCGGCGGGAGGTTTCGTGGTCGGTTTCGGGTTGA
AGTTGGTATTTTAGCGGTAATTTCGAAGGGCGCGGAGTGATAGCGCGTGA
CGGTTTTCGAGACGTTAGTTGTCGTTTTTCGGTTGTGTGGTTTTGATTTTTT
GATTTTTTTACGACGTCGTTGGTTGGGAGATTTATTGGATTTTGCGGTTGG
TTAAAAAGAGAGGGGTAGTTTCGCGTTTTGGGGGTTTTTAGTAGGGGAAG
TGGCGGGTGTTGCGTTGGGTATTTTGTTTGGGGTATTTGTTTGGGATTTTG
TTGGTGTTTTTTATTTGGCGAGGGGTTAGTGGTGGGGGTAGGGGG
[SEQ ID NO: 33]

FIG 1U

TTTTTTATTTTTATTATTGGTTTTTCGTTAGGTGAGAGGTATTAATAGGGTT
TTAGATAGATGTTTTAGATAGGATGTTTAGCGTAATATTCGTTATTTTTTTT
GTTAGGGGTTTTTAGGACGCGGGGTTGTTTTTTTTTTTTTGGTTAGTCGTAG
AGTTTAGTGGGTTTTTTAGTTAGCGACGTCGTGGGAGAATTAGGAAGTTA
AAGTTATATAGTCGAGAAGCGGTAGTTGGCGTTTCGGAGGTCGTTACGCG
TTGTTATTTCGCGTTTTTCGGAGTTGTCGTTAAAATATTAATTTTAATTCGG
GGTCGGTTACGGAGTTTTTCGTCGTTTTTATCGGCGTTTTCGGTATTTTCGG
ATTTTAGCGTTCGCGTTATTTATTTTTTTGCGGTCGTTATTTGTTTGGGTGT
CGGTTTTTTTTTTGTTTGGTCGCGGCGCGTTTTTTTCGTTTTCGTAGTTTTCG
GGTTGTGCGTTTTTTTTTTTTAGTTATAGTTTTAGTTTTTTTTTTTCGGGAGG
GACGTCGTTTTTTTTTTTTTTGGGTCGGTTATTTTTGTTTCGGGGTTTGTTA
GTGGTTTCGGAGTTGTCGGAAGGGTTGGTTATGGTTCGGGGGTTTTGTTTG
TATTTGGAGAAGAGGAAGGATACGGTTCGAGCGGTTTTTCGGTGGAGTTG
GGGCGTTTGAGCGCGGGTTCGGTGGGTTCGCGCGGCGCGGAGTTGGGTAT
AGGGGTCGGCGCGGGTTTTTTCGCGGGTCGCGTTTGGTTTTTTGGCGTTTT
TTTTTGGTCGTTTTCGCGTATTTTCGTTACGTCGGGTTTAGGTTTGCGTAGT
TTTTATATGTTTTGGTTTAGGAGGTT
[SEQ ID NO: 34]

TCGGCGTTTAGGTGACGTTGATTTTGTTGGTTTATCGTTTTGGGGGTTATTT
AATTTTTTAGCGATGTTTTTTAGTTGGGGAGGTTAAGAAGTGTTTCGTTTA
AGGTTTTTTAATATTCGATTTTTAGATTTTTAATTTTGGGTTAGTTATATCG
TAAATTTTTTTAGTTGTTTTTTTTGCGTTTTGCGTTTTTTTTTTACGTTATTT
GTTAGGGAGTCGTTAAATAGTAAGATCGCGCGTTTTGCGGTTTTAGAGTG
CGGATTTCGGTCGCGTGCGGTTTTGATCGCGTCGTTTTATTTTTGGCGGGG
TTACGTACGGACGTTATGGTTGGCGTCGCGGAGTCGGGCGATGCGCGCGG
ATTTTTTCGGGGTTTTGATTGTTTTTGAGTTTTTTTTGCGGGGGGCGTGCGC
GGTTCGTTTTTCGCGGCGTTACGCGGTTTTTTTTCGGTCGGGGATTGGTGC
GTCGGGCGGGGCGGGGCGGGGCGGGATAAAGGCGCGGGGTTTGGTTGCG
CGGGGTTTGCGGGTAGTTTTAATTTTGGGTTCGTAGTTTGCGTTGGGTGCG
TAGGAAGGTTAGTGTGGGGGTCGTTCGATATTTTTTTTCGCGGAGGTGGG
AGTCGAGTTATATTTTGGAGTGGGGATTGGTCGCGGAGCGGGTTGTTTAG
GGTCGGTCGAGGTCGGGGCGAGTTTTGCGCGGCGTTGGAGATTTTGTATT
TTCGGGCGCGTAGGGTTTTCGGTCGTGGTCGTAGAGTTAGGAGGGGCG
GTTTCGGAGTTCGGCGCGGGGAGGGTTTAGGCGTAGTCGGGGTTGGTAGG
GCGCGATATTCGTTTTTTTTTATTTTTGAAAGGGTTTTTTACGTCGAGAAG
AGGGGCGGGTATGGTCGGTTCGGCGAAATCGGTTTGTATAGATTTTGGGA
AGTTATCGTTTGCGGAGGGTGGGATTTTATAGTTTGTTTATTTGTTTAGGT
TGAGATTTCGTGTTTTAGTTTTGGATGTTTTACGGGTTTTTCGTTTCGGGTA
GCGGCGTACGGGAGGAGAAGATTTTCGGTTTGTAGTTAGATTTTTTTTTGA
GATTTTTTTTAGTTTAGGTTTAGAGTTTTGGG
[SEQ ID NO: 35]

FIG 1V

TTTAAAGTTTTAAGTTTGAGTTAGGGAGGGTTTTAGAGGGAGGTTTGATTG
TAGATCGGGAGTTTTTTTTTTTCGTGCGTCGTTGTTCGGGACGAGAAATTC
GTGGGGTATTTAGGATTAGGATACGAGGTTTTAGTTTGGGTAGGTGGATA
AGTTGTGGGGTTTTATTTTTCGTAGGCGATGGTTTTTTAAAGTTTGTATAA
ATCGGTTTCGTCGGGTCGGTTATGTTCGTTTTTTTTTTCGGCGTGGGAAGTT
TTTTTAAAAGTGGAGGGGAGCGAGTGTCGCGTTTTGTTAATTTCGATTGCG
TTTGGGTTTTTTTCGCGTCGGGTTTCGGAGTCGTTTTTTTTGATTTTGCGAT
TACGGTCGGGGATTTTGCGCGCGTTCGGGAATGTAGAGTTTTTAGCGTCG
CGTAGGGTTCGTTTCGATTTCGGTCGGTTTTGGGTAATTCGTTTCGCGGTT
AGTTTTTATTTTAAGATGTGGTTCGGTTTTTATTTTCGCGGGGGGGAAATG
TCGGGCGATTTTTATATTGATTTTTTTGCGTATTTAGCGTAAATTACGAATT
TAGAGTTGGAGTTGTTCGTAGATTTCGCGTAGTTAGATTTCGCGTTTTTAT
TTCGTTTCGTTTCGTTTCGTTCGGCGTATTAATTTTCGGTCGAGGAGGGGT
CGCGTGGCGTCGCGGGGGGCGGGTCGCGTACGTTTTTCGTAGGGAGGATT
TAGGGATAGTTAGGGTTTCGGGAGAGTTCGCGCGTATCGTTCGGTTTCGC
GGCGTTAGTTATGGCGTTCGTGCGTGGTTTCGTTAGGGATGGGGCGACGC
GGTTAGAGTCGTACGCGATCGAAATTCGTATTTTGGAGTCGTAGAGCGCG
CGGTTTTGTTGTTTAGCGGTTTTTTGGTAAGTGACGTGGGGAAGAAACGTA
GGGCGTAGGAGAGATAGTTGGAAAGGTTTGCGGTGTAGTTGGTTTAGGAT
TGAGGGTTTGGAGGTCGGGTGTTGGAAGATTTTGAGCGAGGTATTTTTTG
GTTTTTTTAGTTGGGAGGTATCGTTGAAAAATTAGGTGATTTTTAAGACGG
TAGATTAGTAGAGTTAGCGTTATTTGGGCGTCGG
[SEQ ID NO: 36]

AAAGTTAAGCGTCGTCGTTATTTAAGGTATTGCGTTGATGCGTTGCGGGTC
GATTAGGTGTTTTCGTCGGGGCGTTTTTTTTTACGTAGGAAGGGTTACGTC
GAGAGAGGTAGGTAATAAGGGTACGGTTGGAGGTCGGAAGGTTATTTCGT
TTTCGGCGGGGCGGGCGCGGTTTAGTTTTATTTTTCGGGTACGTTCGGGCG
GGGCGATTGTAGGGAACGGGGCGGGGAGGCGATAGTTTTCGGTTTCGTCG
CGCGTTAGTTCGTTTTCGTTGTTCGGAGGCGTCGTAGGTTTGGGTTTTCGG
ATAGTTGAGTTCGAGCGTCGTTTTTCGAAAGGTGAAGGCGGTTCGGGGAG
GCGGGGACGGTGACGGGGGCGGGGGTCGCGGGCGGTTTTTCGACGGTTGT
CGCGGGGTTAGTTTAAAGTTTTCGATTTTCGGTAGTTGCGTTTTTCGCGCG
GGGCGTCGGAGTAGGGCGGGTTAAGTTGGTTTGCGGTCGCGGCGGGAAG
AAGGGTTAGCGAAGTATTTTCGATCGGGTTTAGGCGTCGGACGTCGGGGG
GCGTTTCGTTGTAATTTTTTTTTGGAAGTTTCGATACGAGTTTCGGTTCGCG
CGCGCGTTTTTTTACGGTTACGCGCGTATTTTGTCGTTCGTATTTTCGCGCG
TTTTTCGTTTATTTTTTTTTTTTTTTTTATTTTTATATTTTAAAATAGGTTA
AGGGGTGGAAGTTATATTTGGTGTAGTTTTCGGTTTTGATGTAAAAGTAGT
TTTTGTTTTTGGTTGCGGGATAGCGTTGTGATTATTCGTAACGGGAGAGTT
GTTGTTAGTCGTTATATCGTGCGGAAAGCGTCGGCGATCGGAGTATTGAT
AATGGTTTGTATAGGGGAGCGGAGAGAAGTTTTTGTTGCGTTTTAGATTC
GTTGTTTCGGCGTTCGTTCGTAGGGAGGAGGGGGCGCGATAGGTCGTTTA
GCGCGTGTTTCGGAGTTCGCGTTCGGGTTTGGTCGTTTGGGTGAGTTTTTG
TTCGTTTTTTGTTTTTTTAGTAGTTCGGGGTGGTTGTTTATTTTGTAAATAG
TTTTGTAATACGATTAAAATAGGCGAGATAGTTA
[SEQ ID NO: 37]

FIG 1W

TGGTTGTTTCGTTTGTTTTGATCGTATTGTAAGGTTGTTTGTAAGGTAAAT
AGTTATTTCGGGTTATTGGAAAGGTAGGGGACGAGTAGGAATTTATTTAG
GCGGTTAGATTCGGGCGCGGGTTTCGGGGTACGCGTTAGACGATTTGTCG
CGTTTTTTTTTTTTTGCGGGCGGGCGTCGAGGTAGCGGATTTAGGGCGTAA
TAGAAGTTTTTTTCGTTTTTTTATGTAGATTATTGTTAGTGTTTCGGTCGT
CGGCGTTTTTCGTACGGTGTGGCGATTGGTAGTAGTTTTTTCGTTGCGAGT
AGTTATAGCGTTGTTTCGTAGTTAGGGGTAAAAGTTGTTTTTGTATTAGAG
TCGAGGGTTGTATTAGGTGTAATTTTTATTTTTTGATTTATTTTAGAGTGTG
AGGATGAAAGGAAGAGGAAAAAATAGACGGAGGGCGCGCGGGGGTGCG
GGCGGTAGGGTGCGCGCGTGGTCGTGGGGGAGCGCGCGCGGGTCGGG
GTTCGTGTCGGGGTTTTTAAAGAGAAGTTGTAGCGAGGCGTTTTTCGGCGT
TCGGCGTTTGGGTTCGGTCGGGGGTGTTTCGTTAGTTTTTTTTTCGTCGCG
GTCGTAGGTTAGTTTGGTTCGTTTTATTTCGGCGTTTCGCGCGGGAAGCGT
AGTTATCGGGGATCGGGGGTTTTGGGTTGGTTTCGCGATAGTCGTCGGGA
GATCGTTCGCGGTTTTCGTTTTCGTTATCGTTTTCGTTTTTTCGGGTCGTTT
TTATTTTTCGGGAGGCGGCGTTCGGGTTTAGTTGTTCGGGAATTTAGGTTT
GCGGCGTTTTCGGGTAGCGAAGGCGGGTTGGCGCGCGGCGGAGTCGGGG
ATTGTCGTTTTTTCGTTTCGTTTTTTGTAATCGTTTCGTTCGAACGTGTTCG
GGAAGTGAGGTTGGGTCGCGTTCGTTTCGTCGGGGACGGGGTGATTTTTC
GGTTTTTAGTCGTGTTTTTGTTGTTTGTTTTTTTCGGCGTGGTTTTTTTGCG
TAGGAGAAGACGTTTCGGCGGGAGTATTTGGTCGGTTCGTAGCGTATTAG
CGTAGTATTTTGGGTGACGACGACGTTTGGTTTT
[SEQ ID NO: 38]

GCGATTTTAGAGGAGTAATCGGGTTTTAATTTTTTGCGTTCGTTTTGTTAT
AATTTTTTTTTATTTATTTTTATTTTATTTTTATAATATTTTTTATTGGGGGG
GTTTTTTGTGTTTCGGATTTTTTTTTTTATGGTTTTTTTAGTCGAAGTCGGG
GGTTTTTTGGGCGGTTTGGAGGGTTTGGGTTAGTAGGTGGGTTCGTATTTT
TTGTTGTTTTTTGTCGGGGAGCGGTCGTCGTTGTTGGGCGAGCGTAGGAGC
GCGGCGGAGCGGAGCGCGCGCGGCGGGTCGGGGGTTGCGTAGTTGGCGT
ATTTGTACGGTATTTTGCGTCGTCGGTAGTTTTATTGTCGTATCGGTTTTTA
TTTGTAGATTTTGTTCGACGGTAGCGTGTAGGGTATTCGGTAGGATTATAG
TTTTTTCGGTACGTATTAGTATTTCGATTTTATTTTTATTTGCGTTTTAGTTC
GGTTTTTCGTTTTTTTTTTTTGTATTTTTTTTTTTGTTTGTTAAGGGCGTTAT
CGTCGCGCGGAGTTCGGAGTTTTTTTGGATTTATTCGGTGTAAGACGTAGG
TTGGGGTTGAAGGGTTGGTTAGAGTAGTCGCGG
[SEQ ID NO: 39]

FIG 1X

TCGCGGTTGTTTTGGTTAGTTTTTTAGTTTTAGTTTGCGTTTTGTATCGGAT
GGGTTTAGGGGAGTTTCGGGTTTCGCGCGGCGATGACGTTTTTGGTAGGT
AAAGAGGGAGGTGTAAGGGGAGGGAACGAGGAGTCGAGTTGGGGCGTA
GATGGGGGTGGGGTCGGGATGTTAGTACGTATCGAAGAGGTTGTGGTTTT
GTCGGGTGTTTTGTACGTTGTCGTCGGGTAGGATTTGTAGGTGGAAGTCG
GTGCGGTAATAGAGTTGTCGGCGGCGTAGGATGTCGTGTAGGTGCGTTAG
TTGCGTAGTTTTCGGTTCGTCGCGCGCGTTTCGTTTCGTCGCGTTTTTGCGT
TCGTTTAGTAGCGGCGGTCGTTTTTCGGTAGGAGGTAATAGGAAATGCGA
ATTTATTTGTTGGTTTAAGTTTTTTAGGTCGTTTAGAAAGTTTTCGATTTCG
GTTAAGGGAGTTATGGAGGGGGAGATTCGGAATATAAAAGATTTTTTTAG
TAAAGAGTGTTGTGGGGGTGGGATGGAGGTGGATAGAGAAAAATTATAG
TAAAACGAGCGTAAAAAGTTAAGGTTCGGTTATTTTTTTGAGGTCGT
[SEQ ID NO: 40]

TATATTTTATTTGTGTCGTATATGTGAAGATATAATTGTAAATCGTTTACG
ATTTTGAGTTAAGATTTTGAGTTTTTTGAGGTTAGGAGATCGTTAGGGAAT
GTGAGTGTTTTAGACGGGCGTTGAGTTTAGTTCGGAGATTTATTTCGTTCG
TAGTAGCGGCGCGGGTTTTAGAGAGTTTCGTATTCGGTCGCGTTTTAGTTA
CGTTGATTCGGTTGTGTTCGTAGTGTCGCGTTGTCGCGTAGTTAGGTGTCG
TCGGGTTGGCGCGGTTATTTATGATTGCGTGGTTGGGTTGGGGGTTCGGG
GTCGGGGAGTAGTCGGGATTCGTCGTTTTTTTTATGATTTTTTCGGGTCGA
ATTACGGGATCGTTACGTTGAAGGTGGCGTCGCGGGTTTTCGGGGTCGCG
CGAGTGTAGGGGTCGTTTTCGGTCGGTCGCGAAGTTCGCGGTATCGATTTT
TCGCGAGATTTCGGCGATTTTTTTTTTCGTTTTCGTTTTTTCGTTTTTTGTTT
TTTTTTAGTTTTGGTGTGGGCGGTTTTCGTTATGGTTGCGTTGCGAAGGTTT
TTGTGGTCGTTATTTCGGGTGTTTTTTTTATTTTGCGTTTATTAGTTTTTTTT
TGGGTCGTGGGGGCGGTTTGCGGTGATTATTTTGGGTTTTTTTGGTCGGTT
TTTTTTTTTTCGAGAGGATGAGGAGAGGGTTGTGGCGGAGGCGGTATGGA
GGCGGCGGCGGCGTTGGGGGGAGTTGAGCGTGGCGGCGGCGGTCGGCGG
GGGGTTGGTCGGTTTGGTATGTTATTAGTTGTACGGGGATTTTAGGGTCGG
TTCGTCGGCGATCGGGCGATTTTTAAAGAGCGCGGTTACGGAGTTCGAGG
ATTCGTTTCGCGGTCGGGGGATGTTGTTTATTTTAGTGGCGGTTGTTAAGG
AGACGGTGAGTGCGCGAGCGCGCGTTATATTTGCGCGGGGGATGTGATTT
TCGTGTCGGGTACGTAGGATTTTGGAGGTTGTGGGGACGGTGTAAGCGTT
GTGGTCGCGGGTGAGGAATTTTTCGTGAGCGAGGTTGATATTTAGGTCGG
ATAGTTTAGGATTCGGTTATTTACGTATTGGGA
[SEQ ID NO: 41]

FIG 1Y

TTTTAATACGTGGGTGATCGGATTTTAGGTTGTTCGGTTTAGGTGTTAGTT
TCGTTTACGGGAAGTTTTTTATTCGCGGTTATAGCGTTTGTATCGTTTTTAT
AGTTTTTAGGGTTTTGCGTATTCGGTACGAAGGTTATATTTTTCGCGTAGG
TGTGACGCGCGTTCGCGTATTTATCGTTTTTTTGGTAGTCGTTATTGGGAT
GGGTAGTATTTTTCGGTCGCGGGGCGGGTTTTCGGGTTTCGTGGTCGCGTT
TTTTGAGGGTCGTTCGGTCGTCGGCGAGTCGGTTTTGGGGTTTTCGTATAG
TTGGTAGTATATTAGGTCGATTAGTTTTTCGTCGGTCGTCGTCGTTACGTTT
AGTTTTTTTTAGCGTCGTCGTCGTTTTTATGTCGTTTTCGTTATAGTTTTTTT
TTTATTTTTTCGGGAGGAGAAGGGTCGGTTAGGAAGGTTTAGGGTGGTTA
TCGTAGGTCGTTTTTACGGTTTAAGGAGGGGTTGGTGAGCGTAGAGTGGA
GGAGATATTCGGGGTGGCGGTTATAAGAGTTTTCGTAGCGTAGTTATAGC
GGAGGTCGTTTATATTAGAGTTGGGAGGGGGTAGAGAACGGAGGGGCGG
GGGCGGGGGGGGGGGTCGTCGAAATTTCGCGAGAAGTCGGTGTCGCGAG
TTTCGCGGTCGGTCGAGAGCGATTTTTATATTCGCGCGGTTTCGGGGATTC
GCGACGTTATTTTTAGCGTAGCGGTTTCGTGGTTCGGTTCGGGAAGATTAT
GGAAGAGGCGGCGGATTTCGGTTGTTTTTCGGTTTCGAATTTTTAGTTTAA
TTACGTAGTTATAAATAATCGCGTTAGTTCGGCGATATTTGGTTACGCGAT
AGCGCGATATTGCGGGTATAGTCGAGTTAGCGTAATTGAGGCGCGGTCGA
GTGCGGGGTTTTTTGGGGTTCGCGTCGTTGTTACGGGCGGGGTGGGTTTTC
GAGTTGGGTTTAGCGTTCGTTTGGGATATTTATATTTTTTAACGGTTTTTTG
ATTTTAGGAAATTTAAGGTTTTGATTTAAGGTCGTGAACGATTTGTAATTG
TATTTTTATATATACGATATAAATGAGGTATA
[SEQ ID NO: 42]

GTTTGGGTACGCGGGATAGGTTGTATTCGTTTGTTAGAGGCGTTTTATCGA
GGCGTTACGGGTGAAGTTTTCGGTTTTATTTACGGGGCGGGGTTTCGGTTC
GGTTCGATTATTGTTCGCGGTGGGGGAGGGGGATGGATTACGTTACGCGT
TAAAGGCGATCGCGATTTTTTTTTTTGTAGGTAGTTTGGAAGGTTTTTTTTTT
TTTTTTACGTTATTTTTTTCGTGGTATTGAAAAGTTTCGTTTTTTTTTTTTAG
TTTCGTTTTTTTCGAGCGTTTTTTTTATTGTTTGGAATGGTGCGGTTTTAGG
TCGCGGGTTACGCGGCGGAGGGGGCGTGGTTTGTTTTCGGTTTAGTCGGTT
TTTTTTTGTTTTTGTTGGAGTTCGGGGAGTGGCGTTGGTTGTTAGAGCGAT
GTCGGGTCGGAGTTGCGTCGTTTTAGTTTTTTTGGTTGTCGTCGTTAGTTGT
GTCGTCGCGTAGTACGCGTCGTCGGTGAGTGAGTTTGAGTCGAGGCGTAG
AGAGGGGCGTGTAGGTGCGGGCGCGGATGGAGGCGTAGGTGTGGCGGCG
CGAGCGGGTATAAGGAATATTTCGTGTTGGGTAGTTTT
[SEQ ID NO: 43]

FIG 1Z

GAAGTTGTTTAGTACGAGGTGTTTTTGTATTCGTTCGCGTCGTTATATTTG
CGTTTTTATTCGCGTTCGTATTTGTACGTTTTTTTTTGCGTTTCGGTTTAAG
TTTATTTATCGGCGGCGCGTGTTGCGCGACGGTATAGTTGACGGCGGTAG
TTAGGAGGATTAAGGCGACGTAATTTCGGTTCGGTATCGTTTTAGTAGTTA
ACGTTATTTTTCGGATTTTAGTAGAGGTAAAGAAGAGTCGGTTGGGTCGG
GGGTAGGTTACGTTTTTTTCGTCGCGTGATTCGCGATTTGGGATCGTATTA
TTTTAGGTAGTAGGGGGAACGTTCGGAGGAGGCGGGATTGGGAGGAGAG
GACGGGGTTTTTTAGTGTTACGAAAAGGGTGGCGTAGAGAAAGAGAGAG
AGTTTTTTAGGTTATTTGTAGAAGGAGAGTCGCGATCGTTTTTGGCGCGTG
GCGTGATTTATTTTTTTTTTTTATCGCGGGTAATAGTCGGATCGAGTCGGA
GTTTCGTTTCGTAGGTGGGGTCGGGAGTTTTATTCGTGGCGTTTCGATGGG
GCGTTTTTAGTAGGCGGGTGTAGTTTGTTTCGCGTATTTAGGT
[SEQ ID NO: 44]

GGTAGTGTAGTTGTGGGAATTTTTTTACGCGTACGAATTTAGTTAACGATT
TTTGATAGATTTTTGGGAGTTTGATTAGAGATGTAAGGGGTGAAGGAGCG
TTTTTTATCGTTAGGGAATTTTGGGGATAGAGCGTTTCGGTCGTTTGATGG
TCGAGGTAGGGTGCGATTTAGGATTTAGGACGGCGTCGGGAATTATATTA
TGGTTCGGATTTTTAAGATTTTAAAGTTCGTCGTCGTTATCGTCGCGGTTTT
GTTGTTAGTGAGTTTCGGTCGCGGTTTTTGGTTGGGGAAGAGCGTATTTGG
CGTCGGGAGGGGGTAGGGAGACGGGGATACGGTAGGGATGTTTGGTTTT
GGTTATTTGCGGTCGGGTATGTTCGGGTAGGACGAATTCGTCGTCGGAGT
TAGGGGAAGAATTGGGTTTTCGGGTTGGGTAGGAGGGATTCGGTCGCGAG
GGAGTAGAGAGGCGGTTTTTTTGGTTGTTTCGAGTTCGCGAAGGGAGGGA
AGTTTAGAATCGAGAGAGGGAGGGAGTTAAGGTGGAATTTATAGAGTG
AGTTTTTTGAAGATATAGAGCGGTTGTTTTTTTTATTAATTAATTAA
[SEQ ID NO: 45]

TTAATTAATTAATGAGAGAGGTAATCGTTTTGTGTTTTTAGGAGGTTTATT
TTATGGGTTTTATTTTGATTTTTTTTTTTTTTCGATTTTGGAATTTTTTTTTTT
TCGCGGGTTCGGGGTAGTTAGGGGGATCGTTTTTTTGTTTTTTCGCGGTCG
GGTTTTTTTTGTTTAGTTCGGGGATTTAGTTTTTTTTTTGATTTCGACGGCG
AGTTCGTTTTGTTCGGATATGTTCGGTCGTAGGTGATTAGGGTTAGGTATT
TTTGTCGTGTTTTCGTTTTTTTGTTTTTTTTCGGCGTTAGGTGCGTTTTTTTT
TAGTTAGGGATCGCGGTCGGGATTTATTGGTAGTAGGATCGCGACGATGA
CGACGACGAATTTTAGGGTTTTGGGGATTCGGGTTATGGTATGGTTTTCGA
CGTCGTTTTGGGTTTTGGGTCGTATTTTGTTTCGGTTATTAGGCGGTCGGG
GCGTTTTGTTTTTAGAGTTTTTTAACGGTAGGAAGCGTTTTTTTATTTTTTG
TATTTTTGGTTAAATTTTTAAAAATTTATTAGAAATCGTTGGTTGAGTTCG
TGCGCGTGGAGAGGTTTTTATAGTTGTATTGTT
[SEQ ID NO: 46]

FIG 1AA

CGTTTGCGGAGGATTGCGTTGACGAGATTTTTATTTATTGTTATTAATTTG
TGGTGGAATTTGTAGTTGTATATTGGATTTGATTCGTTTCGTTTCGAATGA
CGTTTGTTCGGAGGTAGTGAAAGTATAGTCGCGTCGTTTTAAGTTAGTTTG
GATATATAAATTAGTACGCGGTCGGAGAATTTCGTAATTTTTGCGTTTATA
AAATATATCGACGATGTTCGATTTATTTTAAGGGTTGAAATTTACGGGTTT
GAGAGATTATAAGAGCGTTTTTTATCGTTATGGAATAACGGGGATAGAAC
GTTTCGGTCGTTTCGGGGGTTCGGAAAAGGTACGGTTTAGGATTTAGGGA
GGCGCGGGGAGTTAGGTTTGGGTTTCGGGTTTTTAAGATTTTGTGTTCGT
TGTCGTCGCGGTTTTGTTGTTGGTGAGTTTTCGTCGCGGTTTTTGGTTGGG
GAAGAGCGTGTTTGGCGTTTGGAGAGGGTAGGGAGAGAGGGGGATACGG
CGGGGGTGCGTGGTTCGGGTCGTTTGCGGTCGGGTATGTTCGGGTAAGAC
GTATTAGTCGTCGGAGTCGGGGGAAGAGATGGGTTTTCGGGTTGGGTAGG
AGCGATTTGGGTCGTTAGGGAATAGAGCGCGCGTTTTATTTGGTGTAAAT
TTTCGAATTTAGTGGGGGAGGGCGATAAGGAGGGAATTTTCGAGTAAGTT
GCGTGAAGTTACGGAGAGGTCGTCGGATTTTGATTTTGTTTTTTTTTTTTAT
TTTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTC
GTTTAGTTTTTGTTTTAATTTTTTTTTTTTTTGCGTTTTCGAATGAATTTTTA
AAGGCGTTTATTGTAGATCGTTTTGAATTTGCGGTCGGCGAAGAATTTTTT
TGTGGTCGTTGCGGTTTAGTGGTTTCGTTTCGTGCGCGGGAGTCGTCGCGG
GCGTAGTTGGAGAGGTTTTTTTTTTTTTTTAGCGGTTGCGTTTTTACGCGTG
CGGGGTCGTTTATCGTTAATGTTATTGTTTGGGGTTTTTTGGGAAAACGAG
ATTTAGGAGAAGGGAGTTGTGGTATTTG
[SEQ ID NO: 47]

TAAGTGTTATAATTTTTTTTTTTTAAATTTCGTTTTTTTAAGGAATTTTAAA
TAATGGTATTGGCGATGAGCGGTTTCGTACGCGTAGGGGCGTAGTCGTTA
AGGAGGGGAAGGGGTTTTTTAGTTGCGTTCGCGACGATTTTCGCGTACG
GAACGGAATTATTGGGTCGTAGCGATTATAGGGGAGTTTTCGTCGGTCG
TAGGTTTAAAGCGATTTGTAATGAGCGTTTTAGGAATTTATTCGAAGGCG
TAAAAGAAAAAGAAATTAAGGTAGGAATTGAGCGAGGAAGGAAGGGAG
GGAAAGAAAGGAAGAAAGAGAAAAAGAGAAAGAAATAGAAAGTAAGGA
AAGAAAATAAAATTAAAGTTCGACGATTTTTCGTGGTTTTACGTAGTTTA
TTCGGGAATTTTTTTTTTGTCGTTTTTTTTTTATTGGATTCGGGAATTTATAT
TAAGTGGAGCGCGCGTTTGTTTTTGGCGGTTTAGGTCGTTTTTGTTTAAT
TCGGGGATTTATTTTTTTTTTCGATTTCGACGATTGGTGCGTTTTGTTCGGA
TATGTTCGGTCGTAGGCGATTCGGGTTACGTATTTTCGTCGTGTTTTTTTTT
GCGGGGATTTATTAATAGTAGGATCGCGGCGATAACGAGTATAAGGGTTT
TGGGGATTCGGGGTTTAGGTTTGGTTTTTCGCGTTTTTTTGGGTTTTGGGTC
GTGTTTTTTTCGGGTTTTCGAAGCGGTCGGGGCGTTTGTTTTCGTTGTTTT
ATGGCGGTAGGGAACGTTTTTATAGTTTTTAGGTTCGTGGGTTTTAGTTT
TTAAAGTAGATCGGGTATCGTCGGTGTATTTTGTGGGCGTAGAGATTGCG
GGGTTTTTCGGTCGCGTGTTGATTTATGTGTTTAGGTTGATTTGGGGCGGC
GCGGTTGTATTTTTATTGTTTTCGGGTAGGCGTTATTCGGGGCGGGGCGAA
TTAGATTTAATGTGTAATTGTAAATTTTATTATAGGTTGGTGATAATAAAT
AAGAGTTTCGTTAACGTAATTTTTCGTAAGCG
[SEQ ID NO: 48]

FIG 1BB

TGTACGTTTATTGTTTGTTTTTTTTTTTGTACGTTTGGTGGGTTTTATTTTAG
GCGGGTGTTGCGACGGTGGTTATTGCGTTTTTGCGTACGCGGGGGTAGTTT
TCGTCGTTATTTTTTTTGGCGTATATGTTGAGTTTTTATCGCGATTCGTTGT
CGAGGGTAGATATTATTCGTAGTTTATAGGTAGAAGGTAGGTAGTGTCGC
GTGTCGCGTTTTGTTGGGTATTTTCGGGGCGTTTTCGTCGCGTTTAGTTAG
CGGATTCGGGAAGTGTTGTGGGTTGGGGGTTGCGGTTTCGAGTCGGGTTT
GTAGTCGTTCGGGCGTTTCGAGTTTAGGGTTTAGTTTTGCGGGTGTTTTCG
CGTTAGTAGGTTCGGGGTGTAGCGTTGGTGGTTGGGGGCGTATTTACGGT
CGAGTCGGGAAGGGATTTTAGCGTTTAGGGTGTGTTTTCGACGGGGATTA
TTGTTTTTGGGTTTTGGTTTGGGATTGCGCGGAGCGTAGCGCGGAAGGGT
GGGAGTTTTTAATTTTTAGTTTTGTGAAGTTGTTTATTTCGGAGTTTGGGTT
TGCGTATTTGTAGGATAGGTGTAATAAATAATATTTCGTTTATTAGATTGT
GGAAAGCGCGAGATGATAATGCGCGCGAAACGTTTAGCGTAGTATTCGGT
ATAGTTATAGTTAACGGTCGTTGGTATTATTGTAATGGTTTGGTTTTGGCG
CGGGAGTATCGGTAGTTGAGTTGGTAATATCGGGGATTCGGGTTTACGGT
TCGGAGATTAGGGATGGGTTGTTTCGAAGTCGCGAATTGTGGTAGTTTTG
GGTTTTTTAGTCGCGTCGGGGAAGTGTTAAGTGTTTCGTTTAATTTCGGGT
TCGGGGTTATGATTTGTAGGGGAGTGGGTGTTAAGGACGGTAGGGATTTG
AGGGTATCGTTTTCGAGGATTTGGTAGCGCGTTTTGGGTATTTAGCGCGGC
GAGTAGGTGGGTGTTGCGGAGAGGGAGTTTTTTTCGCGTTTTAATTTATAT
TTTGTCGTTTGGGTAGTCGCGGTCGTTTACGTTTTTTTTCGTTTGCGGGGGT
TAGACGGTTTTTTTTGGGGTCGGGGCGTAATTTATAAACGTTAATTTGATT
CGATTTGTCGTTTGTTCGTTTTTTGTGATTTGGTGTCGGGGGTTTTTCGTTT
TCGCGTTTGGGGTTAGATAGTCGGTGATTTTTTTCGGAAGGGTTATTTGGG
GATTAGTTAGATTAGGGGATATTTTCGGGGGCGGGGTAATGAGAAATTTG
TTGGAGTGTTCGGTTTTTTAATCGAAAA
[SEQ ID NO: 49]

FIG 1CC

TTTTCGGTTGAGGGGTCGAGTATTTTAGTAAATTTTTTATTGTTTCGTTTTC
GAGGGTGTTTTTTGGTTTGGTTGGTTTTTAGATGATTTTTTCGGAGAGGGT
TATCGGTTGTTTGATTTTAGGCGCGGGAGCGAAGGGTTTTCGGTATTAGGT
TATAAGGGGCGGGTAGGCGGTAGGTCGGATTAGATTAGCGTTTGTGGATT
GCGTTTCGGTTTTAGGGAGGGTCGTTTGGTTTTCGTAGGCGGAGGGAGGC
GTGGGCGGTCGCGGTTGTTTAGGCGGTAGAATGTGGATTGAGGCGCGGAA
GGGGTTTTTTTTTCGTAGTATTTATTTGTTCGTCGCGTTGGGTGTTTAGAAC
GCGTTGTTAGGTTTTCGAGGGCGATATTTTTAGATTTTTGTCGTTTTTGATA
TTTATTTTTTTGTAAATTATGGTTTCGAATTCGGGGTTAAGCGAGATATTT
GATATTTTTTCGGCGCGGTTGGAGGATTTAAGGTTGTTATAGTTCGCGATT
TCGGGATAGTTTATTTTTGATTTTCGGGTCGTGAGTTCGAATTTTCGATGTT
ATTAGTTTAGTTGTCGATATTTTCGACGTTATATTTCGGGATTTATTTATTT
TTATTCGTAGAAAGAAAAAAAAAATCGTTAAGATTAAATTATTATAGTAAT
ATTAACGATCGTTGATTGTGGTTGTGTCGGGTATTGCGTTGAGCGTTTCGC
GCGTATTGTTATTTCGCGTTTTTTATAGTTTGATAGGCGAGGTGTTATTTAT
TATATTTATTTTATAGATGCGTAGATTTAGGTTTCGGGATAAGTAATTTTA
TAAGATTGGAGATTAGAAGTTTTTATTTTTTCGCGTTGCGTTTCGCGTAAT
TTTAAATTAAAATTTAGAGATAATGGTTTTCGTCGAGGATATATTTTGAAC
GTTAGAATTTTTTTTCGATTCGGTCGTGGATACGTTTTTAGTTATTAACGTT
GTATTTCGAGTTTGTTGACGCGGAGATATTCGTAGAGTTAGGTTTTGGGTT
CGGGACGTTCGGGCGGTTGTAAATTCGGTTCGGAGTCGTAGTTTTTAATTT
ATAGTATTTTTCGAGTTCGTTGGTTGGACGCGGCGGAGGCGTTTCGGGGG
TGTTTAGTAGGGCGCGGTACGCGGTATTGTTTATTTTTTGTTTGTAGGTTG
CGGATGATGTTTGTTTTCGGTAGCGGGTCGCGGTAGAGGTTTAGTATGTAC
GTTAGAGGGGATGGCGACGAGGGTTGTTTTCGCGTACGTAGGAGCGTAGT
GGTTATCGTCGTAGTATTCGTTTGGAGTAGGGTTTATTAGGCGTGTAGAAG
GAAGGGTAGGTAGTGGGCGTGTA
[SEQ ID NO: 50]

TTTTGAAGGGCGGCGGATTTTAGGGTTATGTTGGTTGTTTTTAGAAAGTAG
GAGTTCGAAATCGCGGGGTTAACGAACGTTTATATTTTTTGTTATAATTTC
GTTATTTTTTTGCGTTTTTTTTTTTGTTTTTTGTTTTTATAGGTAACGTTTAG
AACGAGTGTTTTTTTCGGTGGGGTATTGAGGAGTTTGGGTTGTAGTTGTCG
AGTCGTTATAGTTACGTTGAGTTCGGTTTGGTTTGTATATTGGCGTTATCG
TTTGGCGGGGAGCGGGATTGACGCGTTTTTTTTTTTTTTTTTAGTTTAGAT
TACGGAGGCGCGGAGTTTTATTTTTTGTTTTGGGCGAGGGG
[SEQ ID NO: 51]

TTTTTCGTTTAGGGTAGGAGATGGAGTTTCGCGTTTTCGTGATTTGGGTTG
GAGGAGAGGGAGAGGAGCGCGTTAGTTTCGTTTTTCGTTAGGCGGTGGCG
TTAGTGTGTAGGTTAGGTCGGGTTTAGCGTGGTTGTGGCGGTTCGGTAGTT
GTAGTTTAGGTTTTTTAGTATTTTATCGGGAGAAGTATTCGTTTTGGGCGT
TATTTGTGGGGGTAGGGGGTAAGGGGAGAGGCGTAGGGGAGTGGCGAGG
TTGTAGTAGAGAATGTGGGCGTTCGTTGGTTTCGCGGTTTCGGGTTTTTGT
TTTTTGGGGATAGTTAGTATGGTTTTGAAGTTCGTCGTTTTTTAGAG
[SEQ ID NO: 52]

FIG 1DD

TAATTAGGGTTGGTTTATTTTTTTTTAGTTAATTTTTTTTTATTTTTAGTTTT
TAATTTAATTTATTTCGTTTATTAGTTTTTGGATTTTTATTATTTTTTTCGTA
TTTTCGGTAGTTTTGGGGAAGTTTCGTGACGTTATAGGTTTCGTTTTTAGTT
TCGGTTCGGGGTTAGTGCGTGTTGACGTTATGTTGCGTGCGGGTCGGTGCG
GAATCGTTTTTTTAATTTCGCGGGGTAGTAGGAGTTAGTTAGTAAAGAGTC
GAGGTCGGGCGCGCGATTTTCGTTTTTTTGTTTTTGGTCGTATATTTTGCGT
ATATTTTTTTTTTTGTATGGTGGATATTATTTTTTATT
[SEQ ID NO: 53]

AATGAAAAATAATATTTATTATGTAGAAAAAGAGATGTGCGTAAAGTGTG
CGGTTAGGGGTAGAAGGACGAGGGTCGCGCGTTCGGTTTCGGTTTTTTGT
TAATTAATTTTTATTGTTTCGCGGAGTTGAAGGAGCGATTTCGTATCGGTT
CGTACGTAGTATGACGTTAATACGTATTAGTTTCGGGTCGGAGTTGGGGG
CGGGATTTGTGGCGTTACGAAGTTTTTTTAGAATTGTCGGGGATGCGGGG
GAGGTGATGGGGATTTAGGGGTTGATGGGCGGGGTGGGTTGGGTTGGAG
GTTGGGGGTGAAGGGAGATTGGTTGGGAGGAAGTGGGTTAATTTTGATTG
[SEQ ID NO: 54]

FIG 2A

GTCAGGTGGGCTACTCCACCAGGGAGGCCTTCTCCCCACCCCTGGCCCAGGGCCCTTCCG
GATTTCCAGAGAATTCTGGAACCAAGACCTTCCCCTTTCTCACCAGGGACCTCCTTGCTC
CAGGGCCTCCCGAGCGCCTGGCCGTGAGGCAGGGCCCAGAAGGCCAGGGCGGGATCCAGG
TGGCTGGCCTCACCCACTGGGACGTGCCCAACCTGGAGACATTGCACCAGGTAGGGCTGC
ACCGCTCTCCGAGACCCCGCCCCGTGCTTCCACTTGGGGGCGGGGACCCTGCACCTGACC
AGCCCTTCGCCCCGCCTTCCAGATGCTGAAACTGGGGAGGAGCAACCGGGCCACCGCCGC
CACCGCCATGAACCAGCGCAGCTCCCGCTCGCATGCCCTGGTCACGCTGACGCTGCGCGC
GGCGTCTCCACCGCGCGCTCCAGGCACCGCAGGTACCACGGCCGGTGCCTGAGCCCTGCG
GAGTCTCCAGAGCACCCGAGGCCCGGCCTTCCCCCATGTCGGGCTCGCTCGCCCCTCTAG
GCACGCTGCACCTGGTGGACCTGGCGGGATCCGAACGCGCACGGAAGGCAGGGGCGGCCG
GCCCGCCGCGGGGAGACCCAGACGGCGCCCGGCGCCTGCGGGAGGCCCAGACCATAAACC
GCTCGCTGCTGGCGCTAGGAGGCGTGATGGCCGCACTGCGGGCCCACCGGCCGCACGTGC
CCTTCCGCGACTCGCAGCTCACGCGACTGCTGCAGCCGGCGCTGGGCCCAGGCACCACCG
CGGTGCTGCTGCTGCAGGTGGGCGCCGGGGCGGGGCAGGTGTGTGCGTGCCGGTCGCCGC
CCACCCGGGCCCGCCCACCCGCGCCTCTTGCCCGCAGATCTCCACGCGGCCGGAGGATCT
CGGGGAGACAGTCTGCTCCCTCAAGTTCGCCGACCGAGTGGGTCAAGTGGAGCTGGGGCC
AGCCCGGCGCCGCAGGGTCCCGCGCTCCTCCGGGACGCCTTCTTCCCTCAGCACCGACAC
TCCGCTCACCGGGACCCCCTGCACCCCTACGCCGTCCCCTGGCAGTCCTCCATGCCCCAG
TCCCGACAACGGCTCGGGCTCGGCTCTCGCGCCCGCAGAGGGCCTGCCCCTCTAGTCCTG
GGTCGCGGCCCTGCCCATGGGGTCTCAGGCCAGGTCTCTGCTGGCAGAGGCGGTAGTAAA
GTCCCTGTACCCCGTCTCCCAGGGCACAAGCTCCCTAGCCTCTTTGGATCCATTGCCCCT
GAGCTCCCAGAGTCACCCCTCCACCTCCGCAGCCAGTGAA
[SEQ ID NO: 119] - KIFC2

TTCACTGGCTGCGGAGGTGGAGGGGTGACTCTGGGAGCTCAGGGGCAATGGATCCAAAGA
GGCTAGGGAGCTTGTGCCCTGGGAGACGGGGTACAGGGACTTTACTACCGCCTCTGCCAG
CAGAGACCTGGCCTGAGACCCCATGGGCAGGGCCGCGACCCAGGACTAGAGGGGCAGGCC
CTCTGCGGGCGCGAGAGCCGAGCCCGAGCCGTTGTCGGGACTGGGGCATGGAGGACTGCC
AGGGGACGGCGTAGGGGTGCAGGGGGTCCCGGTGAGCGGAGTGTCGGTGCTGAGGGAAGA
AGGCGTCCCGGAGGAGCGCGGGACCCTGCGGCGCCGGGCTGGCCCCAGCTCCACTTGACC
CACTCGGTCGGCGAACTTGAGGGAGCAGACTGTCTCCCCGAGATCCTCCGGCCGCGTGGA
GATCTGCGGGCAAGAGGCGCGGGTGGGCGGGCCCGGGTGGGCGGCGACCGGCACGCACAC
ACCTGCCCCGCCCCGGCGCCCACCTGCAGCAGCAGCACCGCGGTGGTGCCTGGGCCCAGC
GCCGGCTGCAGCAGTCGCGTGAGCTGCGAGTCGCGGAAGGGCACGTGCGGCCGGTGGGCC
CGCAGTGCGGCCATCACGCCTCCTAGCGCCAGCAGCGAGCGGTTTATGGTCTGGGCCTCC
CGCAGGCGCCGGGCGCCGTCTGGGTCTCCCCGCGGCGGGCCGGCCGCCCCTGCCTTCCGT
GCGCGTTCGGATCCCGCCAGGTCCACCAGGTGCAGCGTGCCTAGAGGGGCGAGCGAGCCC
GACATGGGGGAAGGCCGGGCCTCGGGTGCTCTGGAGACTCCGCAGGGCTCAGGCACCGGC
CGTGGTACCTGCGGTGCCTGGAGCGCGCGGTGGAGACGCCGCGCGCAGCGTCAGCGTGAC
CAGGGCATGCGAGCGGGAGCTGCGCTGGTTCATGGCGGTGGCGGCGGTGGCCCGGTTGCT
CCTCCCCAGTTTCAGCATCTGGAAGGCGGGGCGAAGGGCTGGTCAGGTGCAGGGTCCCCG
CCCCCAAGTGGAAGCACGGGGCGGGGTCTCGGAGAGCGGTGCAGCCCTACCTGGTGCAAT
GTCTCCAGGTTGGGCACGTCCCAGTGGGTGAGGCCAGCCACCTGGATCCCGCCCTGGCCT
TCTGGGCCCTGCCTCACGGCCAGGCGCTCGGGAGGCCCTGGAGCAAGGAGGTCCCTGGTG
AGAAAGGGGAAGGTCTTGGTTCCAGAATTCTCTGGAAATCCGGAAGGGCCCTGGGCCAGG
GGTGGGGAGAAGGCCTCCCTGGTGGAGTAGCCCACCTGAC
[SEQ ID NO: 120] - KIFC2

FIG 2B

AACACGTGTAGGTTGTTGGAATTACATTAACGAATGAATGAGCAAAACCTTCTAAACCAC
CGACCAATGAAACCCCGATACAGAAAATCGCTGTCATGAGTAAGTTAGCACTCCTGAAGA
GTTTGAATACTGAACTGGCCAGAGTCTGCGCGCCGACGCCCCCCAGGTGGCCGGAGTGAC
CCGGAGCAGGCGTGGCTGTCTCTCAGACCCGCGCGTTGGGCCCGAACAGTTTGTCCCCAC
GCAGCTCCCATATAAGGCGGGCCCCTCCCCTGCCCCAGCCAGCTAGGTCGCCGCGCTGGC
TCCCTGGCGGCTTCTCAAACCAACCCGCCGCTACTGCGCATGCTTGGCAAGCTCGCCCGC
TCCTTAATATCCTGCTCCGGCTGTTCCTGCCACCCGTTGGTCAAATTCGCACCCAGCTCT
GCTCCAGACAGAGGGAAAACCCAGTGATTTCCGGGCTCTAGAAACAAAGGGAGGCTATGA
TTCCCTGCTGGCCCTAGGGGTCCAGGGAAGGTTATGGAAAGATAATTCTTTGTGTAAGCG
GGTTGCGTAC
[SEQ ID NO: 121] - c20orf23

GTACGCAACCCGCTTACACAAAGAATTATCTTTCCATAACCTTCCCTGGACCCCTAGGGC
CAGCAGGGAATCATAGCCTCCCTTTGTTTCTAGAGCCCGGAAATCACTGGGTTTTCCCTC
TGTCTGGAGCAGAGCTGGGTGCGAATTTGACCAACGGGTGGCAGGAACAGCCGGAGCAGG
ATATTAAGGAGCGGGCGAGCTTGCCAAGCATGCGCAGTAGCGGCGGGTTGGTTTGAGAAG
CCGCCAGGGAGCCAGCGCGGCGACCTAGCTGGCTGGGGCAGGGGAGGGGCCCGCCTTATA
TGGGAGCTGCGTGGGGACAAACTGTTCGGGCCCAACGCGCGGGTCTGAGAGACAGCCACG
CCTGCTCCGGGTCACTCCGGCCACCTGGGGGGCGTCGGCGCGCAGACTCTGGCCAGTTCA
GTATTCAAACTCTTCAGGAGTGCTAACTTACTCATGACAGCGATTTTCTGTATCGGGGTT
TCATTGGTCGGTGGTTTAGAAGGTTTTGCTCATTCATTCGTTAATGTAATTCCAACAACC
TACACGTGTT
[SEQ ID NO: 122] - c20orf23

CAGCCGAGGGGCGCGCCTGGCTGATGTGTGGTTGAATGGAGAGCGGCCCAACCCTCCTCC
TTCCTCCTCTTCTTCTCCCCGCCCTGACACCCGGGCCTCAAACTTCAACCAAAGCCCGTG
CCCTTTTCAATTTACCCCCCTCGATCAAAATGAGCCATTCTTGTCTGTCCTCCGCGGCGG
CCCATTGTCTGGCGTGATAGGTTTGCAGATTTGACAGCTGGGCGCACGCAGATTTGATTC
AAACTCGGTCTCCCCGAGAGATGAACTTGGACATCAGCAAAGATCCCGAGCACTGCCGGC
TGGCTCCTAGACCGGTCTCCCGACCCAGTGTAGACTTCGGTGCCCCGGGCGCCCCCCGGC
GTGCGGGAAGGGGAGCGTGTGTCAGGCGTGGGGGGCGGGGGGTGAGCAGCACGACTGGGA
ACCAGCGGTCCCAGGGGTTGGGGCGAAGGGCTGTGTACATGTTAGGCTTTTTTTGTTGTT
GTTAATTTACTCTCGAAACAGCCAAAATGGAGGTCAGCTTATAAATTTTCTAAAGCCAGG
TCTGGCCGGG
[SEQ ID NO: 123] - GFRA1

CCCGGCCAGACCTGGCTTTAGAAAATTTATAAGCTGACCTCCATTTTGGCTGTTTCGAGA
GTAAATTAACAACAACAAAAAAAGCCTAACATGTACACAGCCCTTCGCCCCAACCCCTGG
GACCGCTGGTTCCCAGTCGTGCTGCTCACCCCCCGCCCCCCACGCCTGACACACGCTCCC
CTTCCCGCACGCCGGGGGGCGCCCGGGGCACCGAAGTCTACACTGGGTCGGGAGACCGGT
CTAGGAGCCAGCCGGCAGTGCTCGGGATCTTTGCTGATGTCCAAGTTCATCTCTCGGGGA
GACCGAGTTTGAATCAAATCTGCGTGCGCCCAGCTGTCAAATCTGCAAACCTATCACGCC
AGACAATGGGCCGCCGCGGAGGACAGACAAGAATGGCTCATTTTGATCGAGGGGGGTAAA
TTGAAAAGGGCACGGGCTTTGGTTGAAGTTTGAGGCCCGGGTGTCAGGGCGGGGAGAAGA
AGAGGAGGAAGGAGGAGGGTTGGGCCGCTCTCCATTCAACCACACATCAGCCAGGCGCGC
CCCTCGGCTG
[SEQ ID NO: 124] - GFRA1

FIG 2C

AGAAACTGAGGTCGGAGTGGGGGCGTGACCAGGCCAGCCTAAGGCCGCTGCACTAATGAG
AAGCTGAGCTCTCAGATTTTTGCCTCCCTGTCCCTGCCAAGTCGCTGTTTCCTGGGACAA
GAGGGAGCCTCACTGAAACGAACTCCGGTCTCAGGGGACAGAATCCTGAAACCCTGGCTC
TGGGGTCCGGGGCAGGGGTGCGCTGCCTCAGGACAGACGGTGAAACTGAGGTCCAGAGCC
GGACATCCACCGCCTGCGGAGGGAACGAGAACGCGGCGCGTCCTGCCTTGCGGGCCGAGC
GGCGCCAGAGCCGCCTCCTCCCGCCCCCCGCGCTAGATCCCCCCGCCCCGTCTTTGCCCT
CGCGACGCCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTGGCT
GCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGT
CAACATCCGGGGCAAACTGGTGTCGCTGGAGAAGTACCGCGGATCGGTGAGTGCGCGGGG
TCTGGCGGCGCCGCTGGGCCCGGCCTCGCCCTGGCGGGGCCTGCTGGGGACGCCCCGCAG
CCCGGTCCCCCGCGCGGTGTGGCTCCGAGGACGCTCCAGCCGCGCGGCCGCCAAACCCCG
GCCCCCGCCCCGCTCGGCCGTGACCTCTGGCGCGGCGCCCCCATCCCGCGCCCGGCCCGG
CCCGGCCCGCGGCTACGTGGCACGGCCTTGGCGCGGAGGAACCCGAAGCGCTCGCAGTCG
GCGCCCACTTCGCTACCGGCACCTTTGGGCAGCGGGGTCCAGACCTTCGCCGGGAGGCCG
GGCACCACTGCCCAGCCTTTGCCATTCACGGGTGAAAAAAGTAACCGTAGCATCGTGCGG
CCTTTCCCTCTCCCGTCCTCATTTTCTGCATCTGGAACGGGGAGTGGCTGATTCGGAGTC
CAGTGAAGAACACTGTGGAGATCAATGTGCAGGGCAGAGAGAGAGTTATTTCAGATGCAC
GGAGACCTCACACGGATCATCCCTGGGAGA
[SEQ ID NO: 125] - GPX7

TCTCCCAGGGATGATCCGTGTGAGGTCTCCGTGCATCTGAAATAACTCTCTCTCTGCCCT
GCACATTGATCTCCACAGTGTTCTTCACTGGACTCCGAATCAGCCACTCCCCGTTCCAGA
TGCAGAAAATGAGGACGGGAGAGGGAAAGGCCGCACGATGCTACGGTTACTTTTTTCACC
CGTGAATGGCAAAGGCTGGGCAGTGGTGCCCGGCCTCCCGGCGAAGGTCTGGACCCCGCT
GCCCAAAGGTGCCGGTAGCGAAGTGGGCGCCGACTGCGAGCGCTTCGGGTTCCTCCGCGC
CAAGGCCGTGCCACGTAGCCGCGGGCCGGGCCGGGCCGGGCGCGGGATGGGGGCGCCGCG
CCAGAGGTCACGGCCGAGCGGGGCGGGGGCCGGGGTTTGGCGGCCGCGCGGCTGGAGCGT
CCTCGGAGCCACACCGCGCGGGGGACCGGGCTGCGGGGCGTCCCCAGCAGGCCCCGCCAG
GGCGAGGCCGGGCCCAGCGGCGCCGCCAGACCCCGCGCACTCACCGATCCGCGGTACTTC
TCCAGCGACACCAGTTTGCCCCGGATGTTGACCGCCTTGAAGTCGTAGAAGTCCTGCTCC
TGCTGCGCGCAGGCCGCAGCCCACAGGAGCAGCCACGCCGCTGCCACCGTCGCCGCCACC
ATGGCTTGTTCCGGAGGTGGCGGCGTCGCGAGGGCAAAGACGGGGCGGGGGGATCTAGCG
CGGGGGGCGGGAGGAGGCGGCTCTGGCGCCGCTCGGCCCGCAAGGCAGGACGCGCCGCGT
TCTCGTTCCCTCCGCAGGCGGTGGATGTCCGGCTCTGGACCTCAGTTTCACCGTCTGTCC
TGAGGCAGCGCACCCCTGCCCCGGACCCCAGAGCCAGGGTTTCAGGATTCTGTCCCCTGA
GACCGGAGTTCGTTTCAGTGAGGCTCCCTCTTGTCCCAGGAAACAGCGACTTGGCAGGGA
CAGGGAGGCAAAAATCTGAGAGCTCAGCTTCTCATTAGTGCAGCGGCCTTAGGCTGGCCT
GGTCACGCCCCCACTCCGACCTCAGTTTCT
[SEQ ID NO: 126] - GPX7

TTCTCTTACGATCTGGCTTTACTCTCACGCGCACAGCCGAGTCCCTGGGGACCCAGCAGA
GGTCCGAAGCGGAGCGGGGCGGGGCGGGGCTACGGAAGCTGGCGAGGCCGAGCCCCTCCT
AGTGCTTCCGGACCTTGCTCCCTGAACACTCGGAGGTGGCGGTGGATCTTACTCCTTCCA
GCCAGTGAGGATCCAGCAACCTGCTCCGTGCCTCCCGCGCCTGTTGGTTGGAAGTGACGA
CCTTGAAGATCGGCCGGTTGGAAGTGACGACCTTGAAGATCGGCGGGCGCAGCGGGGCCG
AGGGGGCGGGTCTGGCGCTAGGTCCAGCCCCTGCGTGCCGGGAACCCCAGAGGAGGTCGC
AGTTCAGCCCAGCTGAGGCCTGTCTGCAGAATCGACACCAACCAGCATCATGTCCATGAC
ACTGGGGTACTGGGACATCCGCGGGGTGAGTGAGGGTCCGCTGCACTGTGGGACCGGGCG
CGTGGGCGGGAAGTGCCGAGCGGCTGGGGACCGGCTCTAGGGACGGTTCCCTCCTTAGGG
CTATCTCTCA
[SEQ ID NO: 127] - GSTM4

FIG 2D

TGAGAGATAGCCCTAAGGAGGGAACCGTCCCTAGAGCCGGTCCCCAGCCGCTCGGCACTT
CCCGCCCACGCGCCCGGTCCCACAGTGCAGCGGACCCTCACTCACCCCGCGGATGTCCCA
GTACCCCAGTGTCATGGACATGATGCTGGTTGGTGTCGATTCTGCAGACAGGCCTCAGCT
GGGCTGAACTGCGACCTCCTCTGGGGTTCCCGGCACGCAGGGGCTGGACCTAGCGCCAGA
CCCGCCCCCTCGGCCCCGCTGCGCCCGCCGATCTTCAAGGTCGTCACTTCCAACCGGCCG
ATCTTCAAGGTCGTCACTTCCAACCAACAGGCGCGGGAGGCACGGAGCAGGTTGCTGGAT
CCTCACTGGCTGGAAGGAGTAAGATCCACCGCCACCTCCGAGTGTTCAGGGAGCAAGGTC
CGGAAGCACTAGGAGGGGCTCGGCCTCGCCAGCTTCCGTAGCCCCGCCCCGCCCCGCTCC
GCTTCGGACCTCTGCTGGGTCCCCAGGGACTCGGCTGTGCGCGTGAGAGTAAAGCCAGAT
CGTAAGAGAA
[SEQ ID NO: 128] - GSTM4

TCTTGAATTGGGGGCGGAGGTAAAAAAAAAAAAAAAGTCCTCACTGTGGGAAGCTATAAA
AAGCAAAGAGGACTGGGGAGAGAGCAGAGAGAGAGAAAGCGGGAGCCCGCGGCGAGCGTA
GCGCAAGTCCGCTCCCTAGGCATCGCTGCGCTGGCAGCGATTCGCTGTCTCTTGTGAGTC
AGGGGACAACGCTTCGGGGCAACTGTGAGTGCGCGTGTGGGGGACCTCGATTCTCTTCAG
ATCTCGAGGATTCGGTCCGGGGACGTCTCCTGATCCCCTACTAAAGCGCCTGCTAACTTT
GAAAAGGAGCACTGTGTCCTGCAAAGTTTGACACATAAAGGATAGGAAAAGAGAGGAGAG
AAAAGCAACTGAGTTGAAGGAGAAGGAGCTGATGCGGGCCTCCTGATCAATTAAGAGGAG
AGTTAAACCGCCGAGATCCCGGCGGGACCAAGGAGGTGCGGGGCAAGAAGGAACGGAAGC
GGTGCGATCCACAGGGCTGGGTTTTCTTGCACCTTGGGTCACGCCTCCTTGGCGAGAAAG
CGCCTCGCAT
[SEQ ID NO: 129] - DKK2

ATGCGAGGCGCTTTCTCGCCAAGGAGGCGTGACCCAAGGTGCAAGAAAACCCAGCCCTGT
GGATCGCACCGCTTCCGTTCCTTCTTGCCCCGCACCTCCTTGGTCCCGCCGGGATCTCGG
CGGTTTAACTCTCCTCTTAATTGATCAGGAGGCCCGCATCAGCTCCTTCTCCTTCAACTC
AGTTGCTTTTCTCTCCTCTCTTTTCCTATCCTTTATGTGTCAAACTTTGCAGGACACAGT
GCTCCTTTTCAAAGTTAGCAGGCGCTTTAGTAGGGGATCAGGAGACGTCCCCGGACCGAA
TCCTCGAGATCTGAAGAGAATCGAGGTCCCCCACACGCGCACTCACAGTTGCCCCGAAGC
GTTGTCCCCTGACTCACAAGAGACAGCGAATCGCTGCCAGCGCAGCGATGCCTAGGGAGC
GGACTTGCGCTACGCTCGCCGCGGGCTCCCGCTTTCTCTCTCTCTGCTCTCTCCCCAGTC
CTCTTTGCTTTTTATAGCTTCCCACAGTGAGGACTTTTTTTTTTTTTTTACCTCCGCCCC
CAATTCAAGA
[SEQ ID NO: 130] - DKK2

CGATTGGCTGCAAGGGTCTCGGCTTGGCCGCGGATTGGTCACACCCGAGGGCTTGAAAGG
TGGCTGGGAGCGCCGGACACCTCAGACGGACGGTGGCCAGGGATCAGGCAGCGGCTCAGG
CGACCCTGAGTGTGCCCCCACCCCGCCATGGCCCGGCTGCTGCAGGCGTCCTGCCTGCTT
TCCCTGCTCCTGGCCGGCTTCGTCTCGCAGAGCCGGGGACAAGAGAAGTCGAAGGTGAGT
GAGCCTCCGGGCCGGGGGCCGGGAGAAAAAACCTAGCCCCTCGGTGTCCAGCGCTCAGTG
CAATGCACCCCTTTTCCCAGGCTCCCCGCCAGATGGGCAATCCCCAGGTGCGAGAGACCT
CCTGAACCCCTTTTGCCGCCCCCTCCGCCGCCGGGACCCCGCCCCCGACCGTCGTCGTCT
CGTAGTTCCATCTGTTGGAGAGCCGAGACCTGGTGCTTCAGGCGGGCAGAATGACTAAGG
GAGGAAGGTCTCTCTCCCCGAGCTCGCACTTTCTCCCCACTGCCACCTCGAGGGTCGCCT
TGCTACATCT
[SEQ ID NO: 131] - GPX3

FIG 2E

AGATGTAGCAAGGCGACCCTCGAGGTGGCAGTGGGGAGAAAGTGCGAGCTCGGGGAGAGA
GACCTTCCTCCCTTAGTCATTCTGCCCGCCTGAAGCACCAGGTCTCGGCTCTCCAACAGA
TGGAACTACGAGACGACGACGGTCGGGGGCGGGGTCCCGGCGGCGGAGGGGGCGGCAAAA
GGGGTTCAGGAGGTCTCTCGCACCTGGGGATTGCCCATCTGGCGGGGAGCCTGGGAAAAG
GGGTGCATTGCACTGAGCGCTGGACACCGAGGGGCTAGGTTTTTTCTCCCGGCCCCCGGC
CCGGAGGCTCACTCACCTTCGACTTCTCTTGTCCCCGGCTCTGCGAGACGAAGCCGGCCA
GGAGCAGGGAAAGCAGGCAGGACGCCTGCAGCAGCCGGGCCATGGCGGGGTGGGGGCACA
CTCAGGGTCGCCTGAGCCGCTGCCTGATCCCTGGCCACCGTCCGTCTGAGGTGTCCGGCG
CTCCCAGCCACCTTTCAAGCCCTCGGGTGTGACCAATCCGCGGCCAAGCCGAGACCCTTG
CAGCCAATCG
[SEQ ID NO: 132] - GPX3

AGGGGAACTGGTATCTCCACAGTAATTACTAGAGCAGCTCTGGGGAACGGAGGGTTGGCT
AAGGAAGAAAAGCTCCCCCAACCCTTGGGGCGAGGGAGCGTTCTCTCAATGGAGCCCCCC
CAACTCCCCTCCACCCCCCACCAGTCTTCCAGGAAAGAGGAATACCCTACCCGGCAGGGC
TGCGAAGGAAGGGGAAATCCAACCAGAGCGAAAGTCGCACGCGGACAGCTCTGCCAGCCC
TTGGAGGCATCCGGCGGTCACCCACGGGACAAAGCGCGGCTGCGGGAGCGCGCGCGGGGC
ATTCCGGACCCGCGTCGAGCTCCGCTCTAGAGGGGGCGGCGGGCGGCGACAAGCCGGAGA
GAGGAAGGGCCAAGGAGCACGGCCCTCCTGTCGGCACCATCAGCGGGAGAGTGGCGAGCG
GACGCCTAGACGGAGGGGCCCTACTCAGACCCCATCGAGCCAGTTCCCAAGCTTTTCCCT
CCGACCTGCTCCCTCCCGGGGCGCGTGAGGGTGCGGGTCGGGGGTGAACCTGGTGTTGGG
GAAAGTGATT
[SEQ ID NO: 133] - RASSF5

AATCACTTTCCCCAACACCAGGTTCACCCCCGACCCGCACCCTCACGCGCCCCGGGAGGG
AGCAGGTCGGAGGGAAAAGCTTGGGAACTGGCTCGATGGGGTCTGAGTAGGGCCCCTCCG
TCTAGGCGTCCGCTCGCCACTCTCCCGCTGATGGTGCCGACAGGAGGGCCGTGCTCCTTG
GCCCTTCCTCTCTCCGGCTTGTCGCCGCCCGCCGCCCCCTCTAGAGCGGAGCTCGACGCG
GGTCCGGAATGCCCCGCGCGCGCTCCCGCAGCCGCGCTTTGTCCCGTGGGTGACCGCCGG
ATGCCTCCAAGGGCTGGCAGAGCTGTCCGCGTGCGACTTTCGCTCTGGTTGGATTTCCCC
TTCCTTCGCAGCCCTGCCGGGTAGGGTATTCCTCTTTCCTGGAAGACTGGTGGGGGTGG
AGGGGAGTTGGGGGGGCTCCATTGAGAGAACGCTCCCTCGCCCCAAGGGTTGGGGGAGCT
TTTCTTCCTTAGCCAACCCTCCGTTCCCCAGAGCTGCTCTAGTAATTACTGTGGAGATAC
CAGTTCCCCT
[SEQ ID NO: 134] - RASSF5

FIG 2F

CGGGCAAAAATGGAGAGCAGGCAGAGGTCACATCCTCCTCCTCTTCCTCACGCTCCCGGG
CTGCGTGCCCACAGGGGCACAGCCCTGTGCGCGGTGCCACCGGGGGCCATCAGGCTGGGT
TAGAGGAAGGCCCGACCTCCGCGCAGCAAAGAAAACAAACACAGATGTGTTTGGCTGGGA
CCGGGAGGGAGAAAGTGGCCCCCTTCCCCCGCCCGCGCGCTCCCCCGGGCGTGAGGCTCT
CCGGGCGGCGCGGGGCGCGGGCGAGGCTGACAGTCCCCGGCGGCCCCTCCTCCCCCACGG
GGTGCGCGCCTGGCCCGGCCCAGCCCCCTCTCCGGGGTTTCCCCGGGTGCTCTCCTCGCT
TTCTCTTTGTCTCTGCTGTTCTTTCTCGGGCTCCCGGGTTCCCACCCGCCTGTGCTCTCC
CTCTCGGGCGTCCGGGCCGGTTCCCTTTAACTTTCTTCTTTCCCGGGGTGAAAACTTTGC
TCGGAGCTGGCGGCAGCTCGCGGACGTTATTGGCCGGCGCCCCGCCCGGCGGCCCCGCCC
CCCGCCCCCGCGCTCCCCTCCGCCCCTCACTCCCAGCGCGAGTGGCGGCGGCGGCGGAGC
CTTCGGGGGCGAGCGCGCGTGTGTGTGAGTGCGCGCCGGCCAGCGTGAGTGTGTGTGCGC
CCCGGGCGCGGGCAGGGCAGCACTCCGAGCTCGGCGGGAGCGGCGGGAGCCGGGCGGCCG
CGTAGTCACTCGGGCGAGAGAGGCGGCGGCGGGGCCGGGACCGGGGCTGGGGCTGGGGCA
GCGGCGGCCGCGCCGGGCATGGAGCTGGCAAGCCCGCGCTGAGGCGGGACGCGCCTGCTA
GCAGCGAGCGAGAGGCTCTCCGGCGACCGGCGCGCGGGCTCCCCGGAGGGGCCAGGCAAA
CTTTTCTTTCTCTTTTGCCCCCTCCAGAGGTAAAGTCCCGAACGCGGACTTTCCGGCGGG
GACGCGATCGGGGGGCATCTGAGAGGGACCCCGGGCTGCGAGACGAAGGGGCGCGGGCCG
TGCAGAGTCGGGGTCCCCCAGCTCTCCTGCGCCCGAAACTTGGGGTGCGAGGGGGGCTGG
TCGCGGACGGGGAGACCGGCTCAGGCATGCCCCTCGGGCGGCGTGGGGGCGGCGGTGGCG
GGGAAGCAGAGCGTTCTCCCGCCGGGCGGGGAAGAAGGGGCGCGAGCGGTGCGGACTTGG
AGGGCCCCGGCTTCGCCGCCCGCGGGACTTTGGGGGAGAGAGGCGGGCAGTCGGCTGCGG
GGTGGGTGCCCAGGAAGCCGGGCGTTCTCCCGCATCTCCGCTCGCCACCCCGCCGAGAGC
TGGAGGGCGCGGGGCGGGCTGGCTGAGCGCAGCTCCCTTCTCTCCGCAGGCGCCTTCTGC
GGCAGGCGGACAGATCCTCGGCGCGGCAGGGCCGGGGCAAGCTGGACGCAGCATGATGCG
CGCAGTGTGGGAGGCGCTGGCGGCGCTGGCGGCGGTGGCGTGCCTGGTGGGCGCGGTGCG
CGGCGGGCCCGGGCTCAGCATGTTCGCGGGCCAGGCGGCGCAGCCCGATCCCTGCTCGGA
CGAGAACGGCCACCCGCGCCGCTGCATCCCGGACTTTGTCAATGCGGCCTTCGGCAAGGA
CGTGCGCGTGTCCAGCACCTGCGGCCGGCCCCCGGCGCGCTACTGCGTGGTGAGCGAGCG
CGGCGAGGAGCGGCTGCGCTCGTGCCACCTCTGCAACGCGTCCGACCCCAAGAAGGCGCA
CCCGCCCGCCTTCCTCACCGACCTCAACAACCCGCACAACCTGACGTGCTGGCAGTCCGA
GAACTACCTGCAGTTCCCGCACAACGTCACGCTCACACTGTCCCTCGGCAAGAAGTTCGA
AGTGACCTACGTGAGCCTGCAGTTCTGCTCGCCGCGGCCCGAGTCCATGGCCATCTACAA
GTCCATGGACTACGGGCGCACGTGGGTGCCCTTCCAGTTCTACTCCACGCAGTGCCGCAA
GATGTACAACCGGCCGCACCGCGCGCCCATCACCAAGCAGAACGAGCAGGAGGCCGTGTG
CACCGACTCGCACACCGACATGCGCCCGCTCTCGGGCGGCCTCATCGCCTTCAGCACGCT
GGACGGGCGGCCCTCGGCGCACGACTTCGACAACTCGCCCGTGCTGCAGGACTGGGTCAC
GGCCACAGACATCCGCGTGGCCTTCAGCCGCCTGCACACGTTCGGCGACGAGAACGAGGA
CGACTCGGAGCTGGCGCGCGACTCGTACTTCTACGCGGTGTCCGACCTGCAGGTGGGCGG
CCGGTGCAAGTGCAACGGCCACGCGGCCCGCTGCGTGCGCGACCGCGACGACAGCCTGGT
GTGCGACTGCAGGCACAACACGGCCGGCCCGGAGTGCGACCGCTGCAAGCCCTTCCACTA
CGACCGGCCCTGGCAGCGCGCCACAGCCCGCGAAGCCAACGAGTGCGTGGGTGAGTGGGG
TGCGGCGGCGGAGCCGGCGGCGGGTGGGGCCGCGGGCGGGAGCTGCTGGGCCTCGCAGCG
GCGAGTTCATAGGAGCGCGGGTCGAGGGAACGGCGGGAGGCGCGTTCGCCGATGCCCGGG
ACCCGGGAGGGCTCAGAGCAGGTCCACTCGCTCGCGTGGCGCTCGTGGTGGACGCCCGAA
TTTGCGCCCAGTGCTCTCTGCGAAGCCAAGAAGCAGCAGGAGAAATGTTCCCGGAGGGG
GTTTGGCAGAACATTTGCAGATAGGTCTCCGCTAACCCTGGATCCAAACGCAAACATTCA
TTGCCTTCCCCCTCGTTGGGTTGGACGCTGGGATTCACCT
[SEQ ID NO: 135] - NTN1

FIG 2G

AGGTGAATCCCAGCGTCCAACCCAACGAGGGGGAAGGCAATGAATGTTTGCGTTTGGATC
CAGGGTTAGCGGAGACCTATCTGCAAATGTTCTGCCAAACCCCCTCCCGGGAACATTTCT
CCTGCTGCTTCTTGGCTTCGCAGAGAGCACTGGGCGCAAATTCGGGCGTCCACCACGAGC
GCCACGCGAGCGAGTGGACCTGCTCTGAGCCCTCCCGGGTCCCGGGCATCGGCGAACGCG
CCTCCCGCCGTTCCCTCGACCCGCGCTCCTATGAACTCGCCGCTGCGAGGCCCAGCAGCT
CCCGCCCGCGGCCCCACCCGCCGCCGGCTCCGCCGCCGCACCCCACTCACCCACGCACTC
GTTGGCTTCGCGGGCTGTGGCGCGCTGCCAGGGCCGGTCGTAGTGGAAGGGCTTGCAGCG
GTCGCACTCCGGGCCGGCCGTGTTGTGCCTGCAGTCGCACACCAGGCTGTCGTCGCGGTC
GCGCACGCAGCGGGCCGCGTGGCCGTTGCACTTGCACCGGCCGCCCACCTGCAGGTCGGA
CACCGCGTAGAAGTACGAGTCGCGCGCCAGCTCCGAGTCGTCCTCGTTCTCGTCGCCGAA
CGTGTGCAGGCGGCTGAAGGCCACGCGGATGTCTGTGGCCGTGACCCAGTCCTGCAGCAC
GGGCGAGTTGTCGAAGTCGTGCGCCGAGGGCCGCCCGTCCAGCGTGCTGAAGGCGATGAG
GCCGCCCGAGAGCGGGCGCATGTCGGTGTGCGAGTCGGTGCACACGGCCTCCTGCTCGTT
CTGCTTGGTGATGGGCGCGCGGTGCGGCCGGTTGTACATCTTGCGGCACTGCGTGGAGTA
GAACTGGAAGGGCACCCACGTGCGCCCGTAGTCCATGGACTTGTAGATGGCCATGGACTC
GGGCCGCGGCGAGCAGAACTGCAGGCTCACGTAGGTCACTTCGAACTTCTTGCCGAGGGA
CAGTGTGAGCGTGACGTTGTGCGGGAACTGCAGGTAGTTCTCGGACTGCCAGCACGTCAG
GTTGTGCGGGTTGTTGAGGTCGGTGAGGAAGGCGGGCGGGTGCGCCTTCTTGGGGTCGGA
CGCGTTGCAGAGGTGGCACGAGCGCAGCCGCTCCTCGCCGCGCTCGCTCACCACGCAGTA
GCGCGCCGGGGGCCGGCCGCAGGTGCTGGACACGCGCACGTCCTTGCCGAAGGCCGCATT
GACAAAGTCCGGGATGCAGCGGCGCGGGTGGCCGTTCTCGTCCGAGCAGGGATCGGGCTG
CGCCGCCTGGCCCGCGAACATGCTGAGCCCGGGCCCGCCGCGCACCGCGCCCACCAGGCA
CGCCACCGCCGCCAGCGCCGCCAGCGCCTCCCACACTGCGCGCATCATGCTGCGTCCAGC
TTGCCCCGGCCCTGCCGCGCCGAGGATCTGTCCGCCTGCCGCAGAAGGCGCCTGCGGAGA
GAAGGGAGCTGCGCTCAGCCAGCCCGCCCCGCGCCCTCCAGCTCTCGGCGGGGTGGCGAG
CGGAGATGCGGGAGAACGCCCGGCTTCCTGGGCACCCACCCCGCAGCCGACTGCCCGCCT
CTCTCCCCCAAAGTCCCGCGGGCGGCGAAGCCGGGGCCCTCCAAGTCCGCACCGCTCGCG
CCCCTTCTTCCCCGCCCGGCGGGAGAACGCTCTGCTTCCCCGCCACCGCCGCCCCCACGC
CGCCCGAGGGGCATGCCTGAGCCGGTCTCCCCGTCCGCGACCAGCCCCCCTCGCACCCCA
AGTTTCGGGCGCAGGAGAGCTGGGGGACCCCGACTCTGCACGGCCCGCGCCCCTTCGTCT
CGCAGCCCGGGGTCCCTCTCAGATGCCCCCCGATCGCGTCCCCGCCGGAAAGTCCGCGTT
CGGGACTTTACCTCTGGAGGGGGCAAAAGAGAAAGAAAAGTTTGCCTGGCCCCTCCGGGG
AGCCCGCGCGCCGGTCGCCGGAGAGCCTCTCGCTCGCTGCTAGCAGGCGCGTCCCGCCTC
AGCGCGGGCTTGCCAGCTCCATGCCCGGCGCGGCCGCCGCTGCCCCAGCCCCAGCCCCGG
TCCCGGCCCCGCCGCCGCCTCTCTCGCCCGAGTGACTACGCGGCCGCCCGGCTCCCGCCG
CTCCCGCCGAGCTCGGAGTGCTGCCCTGCCCGCGCCCGGGGCGCACACACACTCACGCTG
GCCGGCGCGCACTCACACACACGCGCGCTCGCCCCCGAAGGCTCCGCCGCCGCCGCCACT
CGCGCTGGGAGTGAGGGGCGGAGGGGAGCGCGGGGGCGGGGGGCGGGGCCGCCGGGCGGG
GCGCCGGCCAATAACGTCCGCGAGCTGCCGCCAGCTCCGAGCAAAGTTTTCACCCCGGGA
AAGAAGAAAGTTAAAGGAACCGGCCCGGACGCCCGAGAGGGAGAGCACAGGCGGGTGGG
AACCCGGGAGCCCGAGAAAGAACAGCAGAGACAAAGAGAAAGCGAGGAGAGCACCCGGGG
AAACCCCGGAGAGGGGGCTGGGCCGGGCCAGGCGCGCACCCCGTGGGGGAGGAGGGGCCG
CCGGGGACTGTCAGCCTCGCCCGCGCCCCGCGCCGCCCGGAGAGCCTCACGCCCGGGGGA
GCGCGCGGGCGGGGGAAGGGGGCCACTTTCTCCCTCCCGGTCCCAGCCAAACACATCTGT
GTTTGTTTTCTTTGCTGCGCGGAGGTCGGGCCTTCCTCTAACCCAGCCTGATGGCCCCCG
GTGGCACCGCGCACAGGGCTGTGCCCCTGTGGGCACGCAGCCCGGGAGCGTGAGGAAGAG
GAGGAGGATGTGACCTCTGCCTGCTCTCCATTTTTGCCCG
[SEQ ID NO: 136] - NTN1

FIG 2H

GCAGTCCTGTGTGACTGGTGAGACTCTTGTAGGGGCGTTTCTACAACGACGAAACCCTTC
CTAGGCACTCACTCCAACAGAATAACAAGCCCATTTTATTAGTATTTCGTTTTCCATGTA
AAGTTCTGCTCATACGAATATATTTATAATTCTGATTTTTTTACGGCATTGGGGAGCACA
CCGACAGGCTGCTGAACGGTGGCTGGAGATTCGAGGGAAAACGAAGTTCGCCGAGGCGGC
CTCGGGCGGGCAGGTCCCGGGCTCCATCACAGGGCACACGCGGCTACCAGGGACGCAGCC
CCCCAACACACACACACACACACACACACACACACACACACACACACACACCCTCTCCCA
CTCATGCCTGGCAACCCAGCAGAAACTTCGGACTGGGGCAAAACAAGCCCGGGCCCCGGC
GGCACGCGGGGCTAGGCGCGTTCCCGCCAGTACCTGGTCGCGAGGCCGCTCGCGGGGTGC
CCTGCGTGCCCCCCACTCCCGCAGCCCGCGCCCTGCTCGCTCACTGTGGGGGCGCAGCGG
CCAGGCTTCTCTGTTTGTTGTTTAAAGAAATCCTAGGGCGGGCGAGCGGCGGCATCTAGG
GGAGGGGGCGCAGCCAGAATTCCCTTCCAGCAAGCGCGTGAGGGGCATTCTCAACGCAAA
ACCAGACCCAGAAAGTAGTGACCAGCCCTCCTCGGATTACCCTTCATTGGCTCCTCCCTT
GCTCCCCCCACCCTCCAGATTTGCATAAAAAAGGCCAAGAAAACTCTGGCTGTGCCCCAG
CAACGGCTCATTCTGCTCCCCCGGGTCGGAGCCCCCCGGAGCTGCGCGCGGGCTTGCAGC
GCCTCGCCCGCGCTGTCCTCCCGGTGTCCCGCTTCTCCGCGCCCCAGCCGCCGGCTGCCA
GCTTTTCGGGGCCCCGAGTCGCACCCAGCGAAGAGAGCGGGCCCGGGACAAGCTCGAACT
CCGGCCGCCTCGCCCTTCCCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCCAC
GATGCTGCAGGGCCCTGGCTCGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGG
CTCGGCGCGCGGGCTCTTCCTCTTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTG
CAAGCCCATCCCTGCCAACCTGCAGCTGTGCCACGGCATCGAATACCAGAACATGCGGCT
GCCCAACCTGCTGGGCCACGAGACCATGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGAT
CCCGCTGGTCATGAAGCAGTGCCACCCGGACACCAAGAAG
[SEQ ID NO: 137] - SFRP2

CTTCTTGGTGTCCGGGTGGCACTGCTTCATGACCAGCGGGATCCAAGCGCCGGCCTGCTC
CAGCACCTCCTTCATGGTCTCGTGGCCCAGCAGGTTGGGCAGCCGCATGTTCTGGTATTC
GATGCCGTGGCACAGCTGCAGGTTGGCAGGGATGGGCTTGCAATTGCTGCGCTTGTAGGA
GAAGTCGGGCTGGCCAAAGAGGAAGAGCCCGCGCGCCGAGCCCAGGCAGCAGTGCGAGGC
GAGGAAGAGCAGCAGCAGCGAGCCAGGGCCCTGCAGCATCGTGGGCGCGCGACCCCGAGG
GGGCAGAGGGAGCGGAGCCGGGGAAGGGCGAGGCGGCCGGAGTTCGAGCTTGTCCCGGGC
CCGCTCTCTTCGCTGGGTGCGACTCGGGGCCCCGAAAAGCTGGCAGCCGGCGGCTGGGGC
GCGGAGAAGCGGGACACCGGGAGGACAGCGCGGGCGAGGCGCTGCAAGCCCGCGCGCAGC
TCCGGGGGGCTCCGACCCGGGGGAGCAGAATGAGCCGTTGCTGGGGCACAGCCAGAGTTT
TCTTGGCCTTTTTTATGCAAATCTGGAGGGTGGGGGGAGCAAGGGAGGAGCCAATGAAGG
GTAATCCGAGGAGGGCTGGTCACTACTTTCTGGGTCTGGTTTTGCGTTGAGAATGCCCCT
CACGCGCTTGCTGGAAGGGAATTCTGGCTGCGCCCCCTCCCCTAGATGCCGCCGCTCGCC
CGCCCTAGGATTTCTTTAAACAACAAACAGAGAAGCCTGGCCGCTGCGCCCCCACAGTGA
GCGAGCAGGGCGCGGGCTGCGGGAGTGGGGGGCACGCAGGGCACCCCGCGAGCGGCCTCG
CGACCAGGTACTGGCGGGAACGCGCCTAGCCCCGCGTGCCGCCGGGGCCCGGGCTTGTTT
TGCCCCAGTCCGAAGTTTCTGCTGGGTTGCCAGGCATGAGTGGGAGAGGGTGTGTGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTTGGGGGGCTGCGTCCCTGGTAGCCG
CGTGTGCCCTGTGATGGAGCCCGGGACCTGCCCGCCCGAGGCCGCCTCGGCGAACTTCGT
TTTCCCTCGAATCTCCAGCCACCGTTCAGCAGCCTGTCGGTGTGCTCCCCAATGCCGTAA
AAAAATCAGAATTATAAATATATTCGTATGAGCAGAACTTTACATGGAAAACGAAATACT
AATAAAATGGGCTTGTTATTCTGTTGGAGTGAGTGCCTAGGAAGGGTTTCGTCGTTGTAG
AAACGCCCCTACAAGAGTCTCACCAGTCACACAGGACTGC
[SEQ ID NO: 138] - SFRP2

FIG 2I

GCTGCCTTTGTTCTTTGACTACTCAGCCAATTCAGGTCTGAGCTGTTCTTCGACGCCGCC
CTAGATGCGATGATGAAGGTCAGGTGCCCGCATCCCACCCACCGTCCCCTCGCAGGGGCC
CTAGGACCCACCCAGATCCCGCCTGTCTCTCTCCCCGCGGCAGGTTCCGCTGCATCGTGC
ACCCTTTCCGCGAGAAGCTGACCCTGCGGAAGGCGCTCGTCACCATCGCCGTCATCTGGG
CCCTGGCGCTGCTCATCATGTGTCCCTCGGCCGTCACGCTGACCGTCACCCGTGAGGAGC
ACCACTTCATGGTGGACGCCCGCAACCGCTCCTACCCGCTCTACTCCTGCTGGGAGGCCT
GGCCCGAGAAGGGCATGCGCAGGGTCTACACCACTGTGCTCTTCTCGCACATCTACCTGG
CGCCGCTGGCGCTCATCGTGGTCATGTACGCCCGCATCGCGCGCAAGCTCTGCCAGGCCC
CGGGCCCGGCCCCCGGGGGCGAGGAGGCTGCGGACCCGCGAGCATCGCGGCGCAGAGCGC
GCGTGGTGCACATGCTGGTCATGGTGGCGCTGTTCTTCACGCTGTCCTGGCTGCCGCTCT
GGGCGCTGCTGCTGCTCATCGACTACGGGCAGCTCAGCGCGCCGCAGCTGCACCTGGTCA
CCGTCTACGCCTTCCCCTTCGCGCACTGGCTGGCCTTCTTCAACAGCAGCGCCAACCCCA
TCATCTACGGCTACTTCAACGAGAACTTCCGCCGCGGCTTCCAGGCCGCCTTCCGCGCCC
GCCTCTGCCCGCGCCCGTCGGGGAGCCACAAGGAGGCCTACTCCGAGCGGCCCGGCGGGC
TTCTGCACAGGCGGGTCTTCGTGGTGGTGCGGCCCAGCGACTCCGGGCTGCCCTCTGAGT
CGGGCCCTAGCAGTGGGGCCCCCAGGCCCGGCCGCCTCCCGCTGCGGAATGGGCGGGTGG
CTCACCACGGCTTGCCCAGGGAAGGGCCTGGCTGCTCCCACCTGCCCCTCACCATTCCAG
CCTGGGATATCTGA
[SEQ ID NO: 139] - GPR147

TCAGATATCCCAGGCTGGAATGGTGAGGGGCAGGTGGGAGCAGCCAGGCCCTTCCCTGGG
CAAGCCGTGGTGAGCCACCCGCCCATTCCGCAGCGGGAGGCGGCCGGGCCTGGGGGCCCC
ACTGCTAGGGCCCGACTCAGAGGGCAGCCCGGAGTCGCTGGGCCGCACCACCACGAAGAC
CCGCCTGTGCAGAAGCCCGCCGGGCCGCTCGGAGTAGGCCTCCTTGTGGCTCCCCGACGG
GCGCGGGCAGAGGCGGGCGCGGAAGGCGGCCTGGAAGCCGCGGCGGAAGTTCTCGTTGAA
GTAGCCGTAGATGATGGGGTTGGCGCTGCTGTTGAAGAAGGCCAGCCAGTGCGCGAAGGG
GAAGGCGTAGACGGTGACCAGGTGCAGCTGCGGCGCGCTGAGCTGCCCGTAGTCGATGAG
CAGCAGCAGCGCCCAGAGCGGCAGCCAGGACAGCGTGAAGAACAGCGCCACCATGACCAG
CATGTGCACCACGCGCGCTCTGCGCCGCGATGCTCGCGGGTCCGCAGCCTCCTCGCCCCC
GGGGGCCGGGCCCGGGGCCTGGCAGAGCTTGCGCGCGATGCGGGCGTACATGACCACGAT
GAGCGCCAGCGGCGCCAGGTAGATGTGCGAGAAGAGCACAGTGGTGTAGACCCTGCGCAT
GCCCTTCTCGGGCCAGGCCTCCCAGCAGGAGTAGAGCGGGTAGGAGCGGTTGCGGGCGTC
CACCATGAAGTGGTGCTCCTCACGGGTGACGGTCAGCGTGACGGCCGAGGGACACATGAT
GAGCAGCGCCAGGGCCCAGATGACGGCGATGGTGACGAGCGCCTTCCGCAGGGTCAGCTT
CTCGCGGAAAGGGTGCACGATGCAGCGGAACCTGCCGCGGGGAGAGAGACAGGCGGGATC
TGGGTGGGTCCTAGGGCCCCTGCGAGGGGACGGTGGGTGGGATGCGGGCACCTGACCTTC
ATCATCGCATCTAGGGCGGCGTCGAAGAACAGCTCAGACCTGAATTGGCTGAGTAGTCAA
AGAACAAAGGCAGC
[SEQ ID NO: 140] - GPR147

FIG 2J

AGAAAGGTAATATTTGGAGGCCTCCGAGGGACGGGCAGGGGAAAGAGGGATCCTCTGACC
CAGCGGGGGCTGGGAGGATGGCTGTTTTTGTTTTTTCCCACCTAGCCTCGGAATCGCGGA
CTGCGCCCAGTGACGGACTCAAACTTACCCTTCCCTCTGACCCCGCCGTAGGATGACGCC
TCAACCCTCGGGTGCGCCCACTGTCCAAGTGACCCGTGAGACGGAGCGGTCCTTCCCCAG
AGCCTCGGAAGACGAAGTGACCTGCCCCACGTCCGCCCCGCCCAGCCCCACTCGCACACG
GGGGAACTGCGCAGAGGCGGAAGAGGGAGGCTGCCGAGGGGCCCCGAGGAAGCTCCGGGC
ACGGCGCGGGGGACGCAGCCGGCCTAAGAGCGAGTTGGCACTGAGCAAGCAGCGACGGAG
TCGGCGAAAGAAGGCCAACGACCGCGAGCGCAATCGAATGCACAACCTCAACTCGGCACT
GGACGCCCTGCGCGGTGTCCTGCCCACCTTCCCAGACGACGCGAAGCTCACCAAGATCGA
GACGCTGCGCTTCGCCCACAACTACATCTGGGCGCTGACTCAAACGCTGCGCATAGCGGA
CCACAGCTTGTACGCGCTGGAGCCGCCGGCGCCGCACTGCGGGGAGCTGGGCAGCCCAGG
CGGTTCCCCCGGGGACTGGGGGTCCCTCTACTCCCCAGTCTCCCAGGCTGGCAGCCTGAG
TCCCGCCGCGTCGCTGGAGGAGCGACCCGGGCTGCTGGGGGCCACCTTTTCCGCCTGCTT
GAGCCCAGGCAGTCTGGCTT
[SEQ ID NO: 141] - NEUROG3

AAGCCAGACTGCCTGGGCTCAAGCAGGCGGAAAAGGTGGCCCCCAGCAGCCCGGGTCGCT
CCTCCAGCGACGCGGCGGGACTCAGGCTGCCAGCCTGGGAGACTGGGGAGTAGAGGGACC
CCCAGTCCCCGGGGGAACCGCCTGGGCTGCCCAGCTCCCCGCAGTGCGGCGCCGGCGGCT
CCAGCGCGTACAAGCTGTGGTCCGCTATGCGCAGCGTTTGAGTCAGCGCCCAGATGTAGT
TGTGGGCGAAGCGCAGCGTCTCGATCTTGGTGAGCTTCGCGTCGTCTGGGAAGGTGGGCA
GGACACCGCGCAGGGCGTCCAGTGCCGAGTTGAGGTTGTGCATTCGATTGCGCTCGCGGT
CGTTGGCCTTCTTTCGCCGACTCCGTCGCTGCTTGCTCAGTGCCAACTCGCTCTTAGGCC
GGCTGCGTCCCCCGCGCCGTGCCCGGAGCTTCCTCGGGGCCCCTCGGCAGCCTCCCTCTT
CCGCCTCTGCGCAGTTCCCCCGTGTGCGAGTGGGGCTGGGCGGGGCGGACGTGGGGCAGG
TCACTTCGTCTTCCGAGGCTCTGGGGAAGGACCGCTCCGTCTCACGGGTCACTTGGACAG
TGGGCGCACCCGAGGGTTGAGGCGTCATCCTACGGCGGGGTCAGAGGGAAGGGTAAGTTT
GAGTCCGTCACTGGGCGCAGTCCGCGATTCCGAGGCTAGGTGGGAAAAAACAAAAACAGC
CATCCTCCCAGCCCCCGCTGGGTCAGAGGATCCCTCTTTCCCCTGCCCGTCCCTCGGAGG
CCTCCAAATATTACCTTTCT
[SEQ ID NO: 142] - NEUROG3

FIG 2K

TAAAGCTTCCCCAGAGGGAGGAAAGGTGGGGGCGGGGCGGCTGCTGAGGCCCAGGATATA
AGGGCTGGAGGTGCTGCTTTCAGGCCTGGCCAGCCCACCATGCACGCCCACTGCCTGCCC
TTCCTTCTGCACGCCTGGTGGGCCCTACTCCAGGCGGGTGCTGCGACGGTGGCCACTGCG
CTCCTGCGTACGCGGGGGCAGCCCTCGTCGCCATCCCCTCTGGCGTACATGCTGAGCCTC
TACCGCGACCCGCTGCCGAGGGCAGACATCATCCGCAGCCTACAGGCAGAAGGTAGGCAG
TGCCGCGTGCCGCGCCCTGCTGGGCACCCCCGGGGCGCCTCCGCCGCGTCCAGCCAGCGG
ACTCGGGAAGTGCTGTGGGTTGGGGGCTGCGGCTCCGAGCCGGGTTTGCAGCCGCCCGGG
CGTCCCGAGCCCAGGGCCTAGCTCTGCGGGTGTCTCCGCGTCAGCAGGCTCGGGGTGCAG
CGTTGGTGGCTGGGGGCGTATCCACGGCCGAGTCGGGAAGGGATTCTAGCGTTCAGGGTG
TGTCCTCGACGGGGACCATTGTCTCTGGGTTTTGGTTTGGGATTGCGCGGAGCGCAGCGC
GGAAGGGTGGGAGCTTCTAATCTCCAGTCTTGTGAAGTTGCTTATCCCGGAGCCTGGGTC
TGCGCATCTGTAGGATAGGTGTAATAAATAACACCTCGCCTATCAGACTGTGGAAAGCGC
GAGATGACAATGCGCGCGAAACGCTCAGCGCAGTACCCGGCACAGCCACAGTCAACGGTC
GTTGGTATTACTGTAATGGTTTGGTCTTGGCGATTTTTTTTTCTTTCTGCGAGTGAGGGT
GAATGGGTCCCGGGGTGTGACGTCGGGAGTATCGGCAGCTGAGCTGGTAACATCGGGGAT
TCGGGCTCACGGCCCGGAGATCAGGGATGGGCTGTCCCGAAGTCGCGAACTGTGGCAGCC
TTGGGTCCTCCAGCCGCGCCGGGGAAGTGTCAAGTGTCTCGCTTAACCCCGGGTTCGGGG
CCATGATTTGCAGGGGAGTGGGTGTCAAGGACGGCAGGGATCTGAGGGTATCGCCCTCGA
GGACCTGGCAGCGCGTTCTGGGCACCCAGCGCGGCGAGCAGGTGGGTGCTGCGGAGAGGG
AGCCCCTTCCGCGCCTCAATCCACATTCTGCCGCCTGGGCAGCCGCGGCCGCCCACGCCT
CCCTCCGCCTGCGGGGGCCAGACGGCCCTCCCTGGGGCCGGGGCGCAATCCACAAACGCT
AATCTGATCCGACCTGCCGCCTGCCCGCCCCTTGTGACCTGGTGCCGGGGGCCCTTCGCT
CCCGCGCCTGGGGTCAGACAGCCGGTGACCCTCTCCGGAAGGGTCATCTGGGGACCAGCC
AGACCAGGGGACACCCTCGGGGGCGGGGCAATGAGAAATTTGCTGGAGTGCTCGGCCCCT
CAACCGAAAAGCGGCCGGGGATGGAGGGGGCAAAGAAGGGAGGGAGCGCTTTTCCAGTT
CACTCCCTTCTGGAAAGTTCGAGATGTGTGCGGTGATGGACAGGCATCTG
[SEQ ID NO: 143] - NODAL

FIG 2L

CAGATGCCTGTCCATCACCGCACACATCTCGAACTTTCCAGAAGGGAGTGAACTGGAAAA
GCGCTCCCTCCCTTCTTTGCCCCCTCCCATCCCCGGCCGCTTTTCGGTTGAGGGGCCGAG
CACTCCAGCAAATTTCTCATTGCCCCGCCCCCGAGGGTGTCCCCTGGTCTGGCTGGTCCC
CAGATGACCCTTCCGGAGAGGGTCACCGGCTGTCTGACCCCAGGCGCGGGAGCGAAGGGC
CCCCGGCACCAGGTCACAAGGGGCGGGCAGGCGGCAGGTCGGATCAGATTAGCGTTTGTG
GATTGCGCCCCGGCCCCAGGGAGGGCCGTCTGGCCCCCGCAGGCGGAGGGAGGCGTGGGC
GGCCGCGGCTGCCCAGGCGGCAGAATGTGGATTGAGGCGCGGAAGGGGCTCCCTCTCCGC
AGCACCCACCTGCTCGCCGCGCTGGGTGCCCAGAACGCGCTGCCAGGTCCTCGAGGGCGA
TACCCTCAGATCCCTGCCGTCCTTGACACCCACTCCCCTGCAAATCATGGCCCCGAACCC
GGGGTTAAGCGAGACACTTGACACTTCCCCGGCGCGGCTGGAGGACCCAAGGCTGCCACA
GTTCGCGACTTCGGGACAGCCCATCCCTGATCTCCGGGCCGTGAGCCCGAATCCCCGATG
TTACCAGCTCAGCTGCCGATACTCCCGACGTCACACCCCGGGACCCATTCACCCTCACTC
GCAGAAAGAAAAAAAAATCGCCAAGACCAAACCATTACAGTAATACCAACGACCGTTGAC
TGTGGCTGTGCCGGGTACTGCGCTGAGCGTTTCGCGCGCATTGTCATCTCGCGCTTTCCA
CAGTCTGATAGGCGAGGTGTTATTTATTACACCTATCCTACAGATGCGCAGACCCAGGCT
CCGGGATAAGCAACTTCACAAGACTGGAGATTAGAAGCTCCCACCCTTCCGCGCTGCGCT
CCGCGCAATCCCAAACCAAAACCCAGAGACAATGGTCCCCGTCGAGGACACACCCTGAAC
GCTAGAATCCCTTCCCGACTCGGCCGTGGATACGCCCCCAGCCACCAACGCTGCACCCCG
AGCCTGCTGACGCGGAGACACCCGCAGAGCTAGGCCCTGGGCTCGGGACGCCCGGGCGGC
TGCAAACCCGGCTCGGAGCCGCAGCCCCCAACCCACAGCACTTCCCGAGTCCGCTGGCTG
GACGCGGCGGAGGCGCCCCGGGGGTGCCCAGCAGGGCGCGGCACGCGGCACTGCCTACCT
TCTGCCTGTAGGCTGCGGATGATGTCTGCCCTCGGCAGCGGGTCGCGGTAGAGGCTCAGC
ATGTACGCCAGAGGGGATGGCGACGAGGGCTGCCCCCGCGTACGCAGGAGCGCAGTGGCC
ACCGTCGCAGCACCCGCCTGGAGTAGGGCCCACCAGGCGTGCAGAAGGAAGGGCAGGCAG
TGGGCGTGCATGGTGGGCTGGCCAGGCCTGAAAGCAGCACCTCCAGCCCTTATATCCTGG
GCCTCAGCAGCCGCCCCGCCCCCACCTTTCCTCCCTCTGGGGAAGCTTTA
[SEQ ID NO: 144] - NODAL

ACCCCGGGGCGTGGGAGAAGCCCCTGCTTGGGGGGACCGTCTGCTGTTTAGGGGCTCCCC
TTCGACACGTGGGAGGCAAAAGTGCAGAGCGCACCATCATCCAGCTCCGGCCGCACTGCA
CAGCGAGGCCGGCCCGGAGCCCGGATGCTGGGCTCGGTCCCGCCGAGGCTCGGCCTGGCT
GTAAAGCAGAGGGGGGCGAGGGAAGCCGGGCCAGCGGGTGTCGCGGGTAGCCGGCGTCCG
GGACGGGGTGTGGCGCCCAGAGCGCTGCTGCCTCTCGCAGCCAGGAGGCTGGATGTCGGG
TTTGGGTGTCTTCCAGAAGGAGCCGCACTAGCGACGAGGGAAGAGGAACTGGCTTCCCGG
GCAGTCTCCCCCGCCCCAAACTTTTCCTCCTCGCGGAGGGTGGGCGGGCGGAGGGAGGAA
GCGCAGCCGGGGAACGTGGCGCCCGCGTTCCTCCCGCCCGGGGGCTGCGGCTGGGCTGAG
TGTGTCTTTAAATCTGAGCCCCCCGCCCCTCGCGGTGGGGCCGGGACTCGCGGTCCGGGC
GGGGGCGGGCGCGGTGATTGGCGGCCGGGTCGGGTCCGCCCCTCGGCGTTGGGTAGCGGG
GCGCTGGGGAGCAGCGCGGCGCGCACGGGCCGGGGCGCGCAGGTCCCGTCGCCGGTGAGC
ACGGGCTCCCTCTCGCGTGGCCTCGCCGGGTCCGCCTGGCCTGCCCACCTCCGGAGCCAC
CTCTGCCCCCGCATGGGCTGGCGAAGTTGGGAGGAGCGAGCTGGAGCCAGAGCGCGCGCC
GGGCGCGCCCCGTCGCTGCCTGACTCGGCGCCCGCAGTTCGGGCGCAGCACGCCGGCCGC
AGGAGCACGGATGCCCCCCGGAGCCGCGGGCTGGCAGGTACCGAAGTGTCCTGCCCTGGG
GCTGGCGAGGGGAGGGCAAATCTGGAATCCCCCGGGCACCCCCCAGCCCGAGGCTGCTCC
AGACACCAACTCCCCATCCTTTGGAGAGGTGAGGTCCTGGGCCTTCACCCCACACCCGCT
CAGGATTGGTCCCTGGGAGGCAAGAGGGAC
[SEQ ID NO: 145] - PALD

FIG 2M

GTCCCTCTTGCCTCCCAGGGACCAATCCTGAGCGGGTGTGGGGTGAAGGCCCAGGACCTC
ACCTCTCCAAAGGATGGGGAGTTGGTGTCTGGAGCAGCCTCGGGCTGGGGGGTGCCCGGG
GGATTCCAGATTTGCCCTCCCCTCGCCAGCCCCAGGGCAGGACACTTCGGTACCTGCCAG
CCCGCGGCTCCGGGGGGCATCCGTGCTCCTGCGGCCGGCGTGCTGCGCCCGAACTGCGGG
CGCCGAGTCAGGCAGCGACGGGGCGCGCCCGGCGCGCGCTCTGGCTCCAGCTCGCTCCTC
CCAACTTCGCCAGCCCATGCGGGGGCAGAGGTGGCTCCGGAGGTGGGCAGGCCAGGCGGA
CCCGGCGAGGCCACGCGAGAGGGAGCCCGTGCTCACCGGCGACGGGACCTGCGCGCCCCG
GCCCGTGCGCGCCGCGCTGCTCCCCAGCGCCCCGCTACCCAACGCCGAGGGGCGGACCCG
ACCCGGCCGCCAATCACCGCGCCCGCCCCCGCCCGGACCGCGAGTCCCGGCCCCACCGCG
AGGGGCGGGGGGCTCAGATTTAAAGACACACTCAGCCCAGCCGCAGCCCCCGGGCGGGAG
GAACGCGGGCGCCACGTTCCCCGGCTGCGCTTCCTCCCTCCGCCCGCCCACCCTCCGCGA
GGAGGAAAAGTTTGGGGCGGGGGAGACTGCCCGGGAAGCCAGTTCCTCTTCCCTCGTCGC
TAGTGCGGCTCCTTCTGGAAGACACCCAAACCCGACATCCAGCCTCCTGGCTGCGAGAGG
CAGCAGCGCTCTGGGCGCCACACCCCGTCCCGGACGCCGGCTACCCGCGACACCCGCTGG
CCCGGCTTCCCTCGCCCCCCTCTGCTTTACAGCCAGGCCGAGCCTCGGCGGGACCGAGCC
CAGCATCCGGGCTCCGGGCCGGCCTCGCTGTGCAGTGCGGCCGGAGCTGGATGATGGTGC
GCTCTGCACTTTTGCCTCCCACGTGTCGAAGGGGAGCCCCTAAACAGCAGACGGTCCCCC
CAAGCAGGGGCTTCTCCCACGCCCCGGGGT
[SEQ ID NO: 146] - PALD

CCGAAAGGACCCGTCCCAGCGAGCCAGGGCCTGGTTTTCCTTCCGCAGAAGGCGGAGGGA
CCGGAGCGGGCGCGGGCACCCCTGGGCTCTGAGGGGCGCGCTCTGAAGGGCGGCGGACTT
CAGGGCCATGCTGGCTGTCCCCAGAAAGCAGGAGCCCGAAACCGCGGGGCCAACGAACGC
CCACATTCTCTGCTACAACCTCGCCACTCCCCTGCGCCTCTCCCCTTGCCCCCTGCCCCC
ACAGGTAACGCCCAGAACGAGTGCTTCTCCCGGTGGGGTACTGAGGAGCCTGGGCTGCAG
CTGCCGAGCCGCCACAGCCACGCTGAGCCCGGCCTGGCCTGCACACTGGCGCCACCGCCT
GGCGGGGAGCGGGACTGACGCGCTCCTCTCCCTCTCCTCCAGCCCAGATCACGGAGGCGC
GGAGCTCCATCTCCTGCCCTGGGCGAGGGGAGTGAGGGAGACAAAGACTTTGGGCACAAC
ACCCACCACATAGAACCTATTCTCTAGTTGGGAAACAAGTCAAGGCAAAGGCGCACAGAG
TGAAAGTCAG
[SEQ ID NO: 147] - LOC399783

CTGACTTTCACTCTGTGCGCCTTTGCCTTGACTTGTTTCCCAACTAGAGAATAGGTTCTA
TGTGGTGGGTGTTGTGCCCAAAGTCTTTGTCTCCCTCACTCCCCTCGCCCAGGGCAGGAG
ATGGAGCTCCGCGCCTCCGTGATCTGGGCTGGAGGAGAGGGAGAGGAGCGCGTCAGTCCC
GCTCCCCGCCAGGCGGTGGCGCCAGTGTGCAGGCCAGGCCGGGCTCAGCGTGGCTGTGGC
GGCTCGGCAGCTGCAGCCCAGGCTCCTCAGTACCCCACCGGGAGAAGCACTCGTTCTGGG
CGTTACCTGTGGGGGCAGGGGGCAAGGGGAGAGGCGCAGGGGAGTGGCGAGGTTGTAGCA
GAGAATGTGGGCGTTCGTTGGCCCCGCGGTTTCGGGCTCCTGCTTTCTGGGGACAGCCAG
CATGGCCCTGAAGTCCGCCGCCCTTCAGAGCGCGCCCCTCAGAGCCCAGGGGTGCCCGCG
CCCGCTCCGGTCCCTCCGCCTTCTGCGGAAGGAAAACCAGGCCCTGGCTCGCTGGGACGG
GTCCTTTCGG
[SEQ ID NO: 148] - LOC399783

FIG 2N

```
CCCTCCAGTTTGCTGGAGTTGCCGGATTACATTGTTCCTCCCCGGTGTGCGGCGTGAGCT
TCCCCCACCCGAGCGCCCAACAAGTCTCCTTTCTCCAGCCTGCGCGCTGCTGCGCTGAGG
CCGAATGAAGCGCAGCACGGTGCGGGCAGCCCGAGGCCCCGAGGCTGGGCTCTGTCTGTC
TGGGACTGCGCCGTGCCCAGCCTCGGTCCCCTCTCTGTGGGTAAGGATGGTTGAGTCCAG
CCTCCACGGCAGCGGCTCCTTGTGCCACTAGCAGCCCTTCTTCTGCGCTCTCCGCCTTTT
CTCTCTAGACTGGATCTCTCCTCCCCCCCGCGCCCCCCTCCCCGCATCTCCCACTCGCTG
GCTCTCTCTCCAGCTGCCTCCTCTCCAGGTCTCTCCTGGCTGCGCGCGCTCCTCTCCCCG
CTTCTCCCCCTCCCGCAGCCTCGCCGCCTTGGTGCCTTCCTGCCCGGCTCGGCCGGCGCT
CGTCCCCGGCCCCGGCCCCGCCAGCCCGGGTCTCCGCGCTCGGAGCAGCTCAGCCCTGCA
GTGGCTCGGGACCCGATGCTATGAGAGGGAAGCGAGCCGGGCGCCCAGACCTTCAGGAGG
CGTCGGATGCGCGGCGGGTCTTGGGACCGGGCTCTCTCTCCGGCTCGCCTTGCCCTCGGG
TGATTATTTGGCTCCGCTCATAGCCCTGCCTTCCTCGGAGGAGCCATCGGTGTCGCGTGC
GTGTGGAGTATCTGCAGACATGACTGCGTGGAGGAGATTCCAGTCGCTGCTCCTGCTTCT
CGGGCTGCTGGTGCTGTGCGCGAGGCTCCTCACTGCAGCGAAGGGTAAGACGGACTTGCT
CCTGGCCGGGGAGGCGGTAGAGCCCTCGGAGGCCCCGTGTGCGGACGCGAGTGTGCGTTT
TGGGGACCGCAGGGTACGGAGTGGCCGCCTCTGCCCGGCGCTGCTCCATCGCCGAAGCTC
GGGGAACGCGATGCACGGGAGGGAGCTTCCATCGCGCTCTCCCCAGCCCTCCTGGGCCCC
CGCCCCACCCCGCCATTCCTTCCCCCTCTCTTGGGCTCACAGGAGAGATCTCTTTTTCTC
GGCAGTACAGGGTGTCAAGGAGAAAGGAACCCAATACGAGTTGGGCTGGAACTGTGCTCC
GCCGGGGCGGTGTTGCCTCCTCCGAGACGTGGACTCCACGGGTCGGGGTGGCTGAGGGGC
AGTTCCCAGGACTTTCTCCCCGGACCCGACGCGCCTGGGAAAGCGTCCCGGGTGAAGCCG
GCCTGGAAAGTTCGGGCTCTCTACGGGGGTTTTGGTACCAATAGGCAAAGGTCTCCGCCG
GCCCGGCCTCCTCGCACCCATACACCCCATTCCTCCTCTCCTCCTTCCCTCTCCAACGTC
CTCAGCCGGCGAGGAGTAGCTGCCTCTAGAAGGTCGCCCCCGCTTTCCTCTCCCCCGGAC
TTCGCTCCTTGCAAGTTGTAAGGTGTTGGCAAGGTGCGTGAAACAGGCTAGGAGTTCTGG
ACCGGCTTCCAAGTCAGATACATTCACTGTGGGCGCACGGGTATCCTCCT
```

[SEQ ID NO: 149] - CSMD1

```
AGGAGGATACCCGTGCGCCCACAGTGAATGTATCTGACTTGGAAGCCGGTCCAGAACTCC
TAGCCTGTTTCACGCACCTTGCCAACACCTTACAACTTGCAAGGAGCGAAGTCCGGGGGA
GAGGAAAGCGGGGGCGACCTTCTAGAGGCAGCTACTCCTCGCCGGCTGAGGACGTTGGAG
AGGGAAGGAGGAGAGGAGGAATGGGGTGTATGGGTGCGAGGAGGCCGGGCCGGCGGAGAC
CTTTGCCTATTGGTACCAAAACCCCCGTAGAGAGCCCGAACTTTCCAGGCCGGCTTCACC
CGGGACGCTTTCCCAGGCGCGTCGGGTCCGGGGAGAAAGTCCTGGGAACTGCCCCTCAGC
CACCCCGACCCGTGGAGTCCACGTCTCGGAGGAGGCAACACCGCCCCGGCGGAGCACAGT
TCCAGCCCAACTCGTATTGGGTTCCTTTCTCCTTGACACCCTGTACTGCCGAGAAAAAGA
GATCTCTCCTGTGAGCCCAAGAGAGGGGGAAGGAATGGCGGGGTGGGGCGGGGGCCCAGG
AGGGCTGGGGAGAGCGCGATGGAAGCTCCCTCCCGTGCATCGCGTTCCCCGAGCTTCGGC
GATGGAGCAGCGCCGGGCAGAGGCGGCCACTCCGTACCCTGCGGTCCCCAAAACGCACAC
TCGCGTCCGCACACGGGGCCTCCGAGGGCTCTACCGCCTCCCCGGCCAGGAGCAAGTCCG
TCTTACCCTTCGCTGCAGTGAGGAGCCTCGCGCACAGCACCAGCAGCCCGAGAAGCAGGA
GCAGCGACTGGAATCTCCTCCACGCAGTCATGTCTGCAGATACTCCACACGCACGCGACA
CCGATGGCTCCTCCGAGGAAGGCAGGGCTATGAGCGGAGCCAAATAATCACCCGAGGGCA
AGGCGAGCCGGAGAGAGAGCCCGGTCCCAAGACCCGCCGCGCATCCGACGCCTCCTGAAG
GTCTGGGCGCCCGGCTCGCTTCCCTCTCATAGCATCGGGTCCCGAGCCACTGCAGGGCTG
AGCTGCTCCGAGCGCGGAGACCCGGGCTGGCGGGGCCGGGGCCGGGGACGAGCGCCGGCC
GAGCCGGGCAGGAAGGCACCAAGGCGGCGAGGCTGCGGGAGGGGGAGAAGCGGGGAGAGG
AGCGCGCGCAGCCAGGAGAGACCTGGAGAGGAGGCAGCTGGAGAGAGAGCCAGCGAGTGG
GAGATGCGGGGAGGGGGGCGCGGGGGGGAGGAGAGATCCAGTCTAGAGAGAAAAGGCGGA
GAGCGCAGAAGAAGGGCTGCTAGTGGCACAAGGAGCCGCTGCCGTGGAGGCTGGACTCAA
CCATCCTTACCCACAGAGAGGGGACCGAGGCTGGGCACGGCGCAGTCCCAGACAGACAGA
GCCCAGCCTCGGGGCCTCGGGCTGCCCGCACCGTGCTGCGCTTCATTCGGCCTCAGCGCA
GCAGCGCGCAGGCTGGAGAAAGGAGACTTGTTGGGCGCTCGGGTGGGGGAAGCTCACGCC
GCACACCGGGGAGGAACAATGTAATCCGGCAACTCCAGCAAACTGGAGGG
```

[SEQ ID NO: 150] - CSMD1

FIG 20

TCCTCCTTGAGCAGGGAGACCATCGGGGTGCAACCTGGCCGGGGCGGGGAGGAGGTGCAG
GGCATTGCCAGAGCGGGCCTGTCCATGGGCAAGGGACAGCGACCTCCTGGGCCAGGACAT
GTGAGAGCTGCGCAGGCCTGGGCCCGGCGTGGCGGAGGTGCGCGAGAGCGGCCAGAAGAG
GGCGCCAGAGAGCCAGGCGCGGCCCGCGGAGGAGCCCGCGCCGGCCCCTATACCCAGCTC
CGCGCCGCGCGGACCCACCGAGCCCGCGCTCAGACGCCCCAGCTCCACCGAGAGGCCGCT
CGGGCCGTGTCCTTCCTCTTCTCCAGGTGCAGGCAGAGCCCCCGAGCCATGGCCAGCCCT
TCCGGCAGCTCCGAAGCCACTGGCAAGCCCCGAGGCAGGGATGGCCGGCCCAGGAGGGAG
GAGGACGACGTCCCTCCCGAAGAGAAGAGGCTGGGGCTGTAGCTGGAGGGGGGAAGCGCA
CAGCCCGAGGACTGCGAGAACGGGGAGGACGCGCCGCGGCCAGGCAGGGAGGAGACCGGC
ACCCAGACAGGTGGCGACCGCAGAGGAGTAAGTGACGCGGGCGCTGGGGTCCGGGGGTGC
CGGGGGCGCCGGTAGGGGCGGCGGGAGGCTCCGTGGCCGGCCCCGGGTTGAAGTTGGTAT
TTTAGCGGCAACTCCGAAGGGCGCGGAGTGACAGCGCGTGACGGCCTCCGAGACGCCAGC
TGCCGCTTCTCGGCTGTGTGGCTTTGACTTCCTGATTCTCCCACGACGTCGCTGGCTGGG
AGACCCACTGGACTCTGCGGCTGGCCAAAAAGAGAGGGGCAGCCCCGCGTCCTGGGGGCC
CCTAGCAGGGGAAGTGGCGGGTGTTGCGCTGGGCATCCTGTCTGGGGCATCTGTCTGGGA
CCCTGTTGGTGCCTCTCACCTGGCGAGGGGCCAGTGGTGGGGGTAGGGGGGAAGTCCCTG
GCGCCAGGCTTGGCCAAGCCCTGCTTGGCTGGACTGCGGGCTGGCGGCGCTCACCCAGCT
CCTCACCTGTCCCGCATCTTCCTGTTTTTC
[SEQ ID NO: 151] - LOC441320

GAAAAACAGGAAGATGCGGGACAGGTGAGGAGCTGGGTGAGCGCCGCCAGCCCGCAGTCC
AGCCAAGCAGGGCTTGGCCAAGCCTGGCGCCAGGGACTTCCCCCCTACCCCCACCACTGG
CCCCTCGCCAGGTGAGAGGCACCAACAGGGTCCCAGACAGATGCCCCAGACAGGATGCCC
AGCGCAACACCCGCCACTTCCCCTGCTAGGGGCCCCCAGGACGCGGGGCTGCCCCTCTCT
TTTTGGCCAGCCGCAGAGTCCAGTGGGTCTCCCAGCCAGCGACGTCGTGGGAGAATCAGG
AAGTCAAAGCCACACAGCCGAGAAGCGGCAGCTGGCGTCTCGGAGGCCGTCACGCGCTGT
CACTCCGCGCCCTTCGGAGTTGCCGCTAAAATACCAACTTCAACCCGGGGCCGGCCACGG
AGCCTCCCGCCGCCCCTACCGGCGCCCCCGGCACCCCCGGACCCCAGCGCCCGCGTCACT
TACTCCTCTGCGGTCGCCACCTGTCTGGGTGCCGGTCTCCTCCCTGCCTGGCCGCGGCGC
GTCCTCCCCGTTCTCGCAGTCCTCGGGCTGTGCGCTTCCCCCCTCCAGCTACAGCCCCAG
CCTCTTCTCTTCGGGAGGGACGTCGTCCTCCTCCCTCCTGGGCCGGCCATCCCTGCCTCG
GGGCTTGCCAGTGGCTTCGGAGCTGCCGGAAGGGCTGGCCATGGCTCGGGGGCTCTGCCT
GCACCTGGAGAAGAGGAAGGACACGGCCCGAGCGGCCTCTCGGTGGAGCTGGGGCGTCTG
AGCGCGGGCTCGGTGGGTCCGCGCGGCGCGGAGCTGGGTATAGGGGCCGGCGCGGGCTCC
TCCGCGGGCCGCGCCTGGCTCTCTGGCGCCCTCTTCTGGCCGCTCTCGCGCACCTCCGCC
ACGCCGGGCCCAGGCCTGCGCAGCTCTCACATGTCCTGGCCCAGGAGGTCGCTGTCCCTT
GCCCATGGACAGGCCCGCTCTGGCAATGCCCTGCACCTCCTCCCCGCCCCGGCCAGGTTG
CACCCCGATGGTCTCCCTGCTCAAGGAGGA
[SEQ ID NO: 152] - LOC441320

FIG 2P

CCCAGTAAGTCACCAATTAAGTCTTTACTACTTAAAAGCAAAATCCACCTATGTCCTGAA
CAGTATCCACTTTACGAGCCTCATTATATGTACGAGATAAAATTCAGAAATAAATAAATA
TACATGTATACGTATACAAATATATTTCAAATTAAAAAATACTTTTAGATAGTGGTATGT
ATTACATTTAGAAATTAATAACGAAGTAAATTATGGGATGTCATCCACGCCTGTCCCAAA
GGTACCGAATTTATAAATCATCTCAGGTGCGGAGCAGGACAGGTTGAAAATAGGAATGAC
ATGAACCCGCGCGGAACAGCTGCCGGCGCGGTGTCCAGGGCGGCACCCCGCCCGGTCCCG
GCCCCTCCAGCCCTGGGCCCGACCCCTACTACGCCTCTGCCTCGACGCGAACGCGGAGCC
CGAGCGCGCGTCACGCCGTGTGGGGCCGAAGAGGCTGCTACCCAGAGGCGGAGTGCGGGC
TCGCGAGGGTCCCCACCCGACTCTCGCTCCCGCCAGCACCTACGGACTCGCGTCCCCGCC
GCGCGCCGACTCGGGAGCAGCACCGCCCCCGGCACAGGAGCCTCACGCGCCTCTTACCTA
ACAGGAAGTTGGGTGGAAGCAGCGCGGACCCACGGCACACCGAACGCACTCCAACAGAAC
CCGACGCAGACACGCGCTTTCAACCGGCGGAGACACTGGCAGGGCCAGAAACGCGCGCAG
CGGGGGCGGGAGGTCGGTAAGCTCCCCGCCCCTGCCCGAGACCCCGCCCCGGCCCGGCCC
CGCCTTTTTCTCTGCCTCCCCTCCCTGCACGTACGGGCCCCGCCCCTCGCGCGACGTTTT
TTGTTGACCCGGAAACGGATTCTCCGGAGCCGAGGTCCGCTCGGGTGAGTGCCCTCCGCT
TTTTGTGGCCAAACCCAGCCACGCAGTTCCCTTCCTGCGGCGTCCTCCACACCCGGGGTC
TGCTGGTCTCCGCGGATGTCACAGGCTCGGCAACCGCCCTCCTGTCGGCGGGGAGTCCCG
CGACGCCCGGAAATGCTCCGAAGCCTGTCGCCCAGCTGCCAGATCTGCGTCTGTGTCCGG
TTCCGTCACTGAGGTCGCCCCTGTCCGGCCCTTCCACCCTAGTTCTCTTCACCGTCCGCC
CATCCTATCGCGCGCGGCCTCAGGTCCCGATTCGGCATGTGGCTTGTCTTCCATCGTCCC
CACCCTCGCCCCTCTTGGCCCCTCAGGGCAGCCCTGGGATTCGGCAGACGCCAGTCCTCC
CTGAGATGCTTCCCCATCCTTCCCTCCGCCAGGCCCTACG
[SEQ ID NO: 153] - ZNF596

CGTAGGGCCTGGCGGAGGGAAGGATGGGGAAGCATCTCAGGGAGGACTGGCGTCTGCCGA
ATCCCAGGGCTGCCCTGAGGGGCCAAGAGGGGCGAGGGTGGGGACGATGGAAGACAAGCC
ACATGCCGAATCGGGACCTGAGGCCGCGCGCGATAGGATGGGCGGACGGTGAAGAGAACT
AGGGTGGAAGGGCCGGACAGGGGCGACCTCAGTGACGGAACCGGACACAGACGCAGATCT
GGCAGCTGGGCGACAGGCTTCGGAGCATTTCCGGGCGTCGCGGGACTCCCCGCCGACAGG
AGGGCGGTTGCCGAGCCTGTGACATCCGCGGAGACCAGCAGACCCCGGGTGTGGAGGACG
CCGCAGGAAGGGAACTGCGTGGCTGGGTTTGGCCACAAAAAGCGGAGGGCACTCACCCGA
GCGGACCTCGGCTCCGGAGAATCCGTTTCCGGGTCAACAAAAAACGTCGCGCGAGGGGCG
GGGCCCGTACGTGCAGGGAGGGGAGGCAGAGAAAAAGGCGGGGCCGGGCCGGGGCGGGGT
CTCGGGCAGGGGCGGGGAGCTTACCGACCTCCCGCCCCCGCTGCGCGCGTTTCTGGCCCT
GCCAGTGTCTCCGCCGGTTGAAAGCGCGTGTCTGCGTCGGGTTCTGTTGGAGTGCGTTCG
GTGTGCCGTGGGTCCGCGCTGCTTCCACCCAACTTCCTGTTAGGTAAGAGGCGCGTGAGG
CTCCTGTGCCGGGGGCGGTGCTGCTCCCGAGTCGGCGCGCGGCGGGGACGCGAGTCCGTA
GGTGCTGGCGGGAGCGAGAGTCGGGTGGGGACCCTCGCGAGCCCGCACTCCGCCTCTGGG
TAGCAGCCTCTTCGGCCCCACACGGCGTGACGCGCGCTCGGGCTCCGCGTTCGCGTCGAG
GCAGAGGCGTAGTAGGGGTCGGGCCCAGGGCTGGAGGGGCCGGGACCGGGCGGGGTGCCG
CCCTGGACACCGCGCCGGCAGCTGTTCCGCGCGGGTTCATGTCATTCCTATTTTCAACCT
GTCCTGCTCCGCACCTGAGATGATTTATAAATTCGGTACCTTTGGGACAGGCGTGGATGA
CATCCCATAATTTACTTCGTTATTAATTTCTAAATGTAATACATACCACTATCTAAAAGT
ATTTTTTAATTTGAAATATATTTGTATACGTATACATGTATATTTATTTATTTCTGAATT
TTATCTCGTACATATAATGAGGCTCGTAAAGTGGATACTGTTCAGGACATAGGTGGATTT
TGCTTTTAAGTAGTAAAGACTTAATTGGTGACTTACTGGG
[SEQ ID NO: 154] - ZNF596

FIG 2Q

ACCGGCGTCCCGCTGGGGGCGCGCGAGCCCCACCCCCAGAGATGCTGACTCAGCAAGTCG
GGAGGGGTTGGGGGTGGGACCTGCCAATCTGCATTTCCAACCGGCGCCCAGGTGACGCTG
ACTCTGCTGGTCTACCGTCTTGGGGGTCACCTAATTTTTCAGCGATGCCTCCCAGCTGGG
GAGGCCAAGAAGTGCCTCGCTCAAGGTCTTCCAACACCCGACCTCCAGACCCTCAATCCT
GGGCCAGCTACACCGCAAACCTTTCCAGCTGTCTCTCCTGCGCCCTGCGTTTCTTCCCCA
CGTCACTTGCCAGGGAGCCGCTAAACAGCAAGACCGCGCGCTCTGCGGCTCCAGAGTGCG
GATTTCGGTCGCGTGCGGCTCTGACCGCGTCGCCCCATCCCTGGCGGGGCCACGCACGGA
CGCCATGGCTGGCGCCGCGGAGCCGGGCGATGCGCGCGGACTCTCCCGGGGCCCTGACTG
TCCCTGAGTCCTCCCTGCGGGGGGCGTGCGCGGCCCGCCCCCCGCGGCGCCACGCGGCCC
CTCCTCGGCCGGGGATTGGTGCGCCGGGCGGGGCGGGGCGGGGCGGGATAAAGGCGCGGG
GTCTGGCTGCGCGGGGTCTGCGGGCAGCTCCAACTCTGGGTTCGTAGTTTGCGCTGGGTG
CGCAGGAAGGTCAGTGTGGGGGTCGCCCGACATTTCCCCCCCGCGGAGGTGGGAGCCGAG
CCACATCTTGGAGTGGGGACTGGCCGCGGAGCGGGTTGCCCAGGGCCGGCCGAGGTCGGG
GCGAGCCCTGCGCGGCGCTGGAGACTCTGCATTCCCGGGCGCGCGCAGGGTCCCCGGCCG
TGGTCGCAGAGTCAGGAGGGGCGGCTCCGGAGCCCGGCGCGGGGAGGGCCCAGGCGCAGT
CGGGGTTGGCAGGGCGCGACACTCGCTCCCCTCCACTTTTGAAAGGGCTTCCCACGCCGA
GAAGAGGGGCGGGCATGGCCGGCCCGGCGAAACCGGTTTGTACAGACTTTGGGAAGCCAT
CGCCTGCGGAGGGTGGGACCCCACAGCTTGTCCACCTGCCCAGGCTGAGACCTCGTGTCC
TAGTCCTGGATGCCCCACGGGTTTCTCGTCCCGGGCAGCGGCGCACGGGAGGAGAAGACT
CCCGGTCTGCAGTCAGACCTCCCTCTGAGACCCTCCCTAGCTCAGGCTTAGAGCTTTGGG
ATTTTTCTCGATCCTTTCTAGCTTTCAGATCATCCCCACGTAAAGTTCAGACTTTACCAG
CCCAGAGAGTTTAAAAAAAAAAAAAAGAGAGAGAGAGAAAG
[SEQ ID NO: 155] - TDH

CTTTCTCTCTCTCTCTTTTTTTTTTTTTTAAACTCTCTGGGCTGGTAAAGTCTGAACTTTA
CGTGGGGATGATCTGAAAGCTAGAAAGGATCGAGAAAAATCCCAAAGCTCTAAGCCTGAG
CTAGGGAGGGTCTCAGAGGGAGGTCTGACTGCAGACCGGGAGTCTTCTCCTCCCGTGCGC
CGCTGCCCGGGACGAGAAACCCGTGGGGCATCCAGGACTAGGACACGAGGTCTCAGCCTG
GGCAGGTGGACAAGCTGTGGGGTCCCACCCTCCGCAGGCGATGGCTTCCCAAAGTCTGTA
CAAACCGGTTTCGCCGGGCCGGCCATGCCCGCCCCTCTTCTCGGCGTGGGAAGCCCTTTC
AAAAGTGGAGGGGAGCGAGTGTCGCGCCCTGCCAACCCCGACTGCGCCTGGGCCCTCCCC
GCGCCGGGCTCCGGAGCCGCCCCTCCTGACTCTGCGACCACGGCCGGGGACCCTGCGCGC
GCCCGGGAATGCAGAGTCTCCAGCGCCGCGCAGGGCTCGCCCCGACCTCGGCCGGCCCTG
GGCAACCCGCTCCGCGGCCAGTCCCCACTCCAAGATGTGGCTCGGCTCCCACCTCCGCGG
GGGGGAAATGTCGGGCGACCCCCACACTGACCTTCCTGCGCACCCAGCGCAAACTACGAA
CCCAGAGTTGGAGCTGCCCGCAGACCCCGCGCAGCCAGACCCCGCGCCTTTATCCCGCCC
CGCCCCGCCCCGCCCGGCGCACCAATCCCCGGCCGAGGAGGGGCCGCGTGGCGCCGCGGG
GGGCGGGCCGCGCACGCCCCCCGCAGGGAGGACTCAGGGACAGTCAGGGCCCCGGGAGAG
TCCGCGCGCATCGCCCGGCTCCGCGGCGCCAGCCATGGCGTCCGTGCGTGGCCCCGCCAG
GGATGGGGCGACGCGGTCAGAGCCGCACGCGACCGAAATCCGCACTCTGGAGCCGCAGAG
CGCGCGGTCTTGCTGTTTAGCGGCTCCCTGGCAAGTGACGTGGGGAAGAAACGCAGGGCG
CAGGAGAGACAGCTGGAAAGGTTTGCGGTGTAGCTGGCCCAGGATTGAGGGTCTGGAGGT
CGGGTGTTGGAAGACCTTGAGCGAGGCACTTCTTGGCCTCCCCAGCTGGGAGGCATCGCT
GAAAAATTAGGTGACCCCCAAGACGGTAGACCAGCAGAGTCAGCGTCACCTGGGCGCCGG
TTGGAAATGCAGATTGGCAGGTCCCACCCCCAACCCCTCCCGACTTGCTGAGTCAGCATC
TCTGGGGGTGGGGCTCGCGCGCCCCCAGCGGGACGCCGGT
[SEQ ID NO: 156] - TDH

FIG 2R

CTCATTTCGGGCCGCTTTTCTCAGAGGGCAAAGATGGGTCAGGGTGGGATGTTACATTAG
TGTTGAGACTCTTTGGATCCGTTTCGTGGGTACCGAGGACGCCTGGGTACGCGGACAGG
CTGCACCCGCCTGCTAGAGGCGCCCCATCGAGGCGCCACGGGTGAAGCTCCCGGCCCCAC
CTACGGGGCGGGGCTCCGGCTCGGTCCGACTATTGCCCGCGGTGGGGGAGGGGGATGGAT
CACGCCACGCGCCAAAGGCGATCGCGACTCTCCTTCTGCAGGTAGCCTGGAAGGCTCTCT
CTCTTTCTCTACGCCACCCTTTTCGTGGCACTGAAAAGCCCCGTCCTCTCCTCCCAGTCC
CGCCTCCTCCGAGCGTTCCCCCTACTGCCTGGAATGGTGCGGTCCCAGGTCGCGGGTCAC
GCGGCGGAGGGGGCGTGGCCTGCCCCCGGCCCAGCCGGCTCTTCTTTGCCTCTGCTGGAG
TCCGGGGAGTGGCGTTGGCTGCTAGAGCGATGCCGGGCCGGAGTTGCGTCGCCTTAGTCC
TCCTGGCTGCCGCCGTCAGCTGTGCCGTCGCGCAGCACGCGCCGCCGGTGAGTGAGCTTG
AGCCGAGGCGCAGAGAGGGGCGTGCAGGTGCGGGCGCGGATGGAGGCGCAGGTGTGGCGG
CGCGAGCGGGTACAAGGAACACCTCGTGCTGGGCAGCTTCTTTACGGGGGTCTGTGGTTT
CGTGCACAGGGGTGTGGGTGCAGAGCGGGCTGGCGAACCCCGTCCTCGGTAGATTCGGTG
CTACCTGCAACTAGAACTCC
[SEQ ID NO: 157] - ASAH1

GGAGTTCTAGTTGCAGGTAGCACCGAATCTACCGAGGACGGGGTTCGCCAGCCCGCTCTG
CACCCACACCCCTGTGCACGAAACCACAGACCCCCGTAAAGAAGCTGCCCAGCACGAGGT
GTTCCTTGTACCCGCTCGCGCCGCCACACCTGCGCCTCCATCCGCGCCCGCACCTGCACG
CCCCTCTCTGCGCCTCGGCTCAAGCTCACTCACCGGCGGCGCGTGCTGCGCGACGGCACA
GCTGACGGCGGCAGCCAGGAGGACTAAGGCGACGCAACTCCGGCCCGGCATCGCTCTAGC
AGCCAACGCCACTCCCCGGACTCCAGCAGAGGCAAAGAAGAGCCGGCTGGGCCGGGGGCA
GGCCACGCCCCCTCCGCCGCGTGACCCGCGACCTGGGACCGCACCATTCCAGGCAGTAGG
GGGAACGCTCGGAGGAGGCGGGACTGGGAGGAGAGGACGGGGCTTTTCAGTGCCACGAAA
AGGGTGGCGTAGAGAAAGAGAGAGAGCCTTCCAGGCTACCTGCAGAAGGAGAGTCGCGAT
CGCCTTTGGCGCGTGGCGTGATCCATCCCCCTCCCCCACCGCGGGCAATAGTCGGACCGA
GCCGGAGCCCCGCCCCGTAGGTGGGGCCGGGAGCTTCACCCGTGGCGCCTCGATGGGGCG
CCTCTAGCAGGCGGGTGCAGCCTGTCCCGCGTACCCAGGCGTCCTCGGTACCCACGAAAC
GGATCCAAAGAGTCTCAACACTAATGTAACATCCCACCCTGACCCATCTTTGCCCTCTGA
GAAAAGCGGCCCGAAATGAG
[SEQ ID NO: 158] - ASAH1

TTCTGCAGAGCCAGCAGCCGGCTCCCACCTACCCAAGGAGAGAAGATCGCTCCAAGACAG
TGAGAGCTTCCCTGCCATTTCAGTGCAAAGTCCCTCCGGAGCGACCTCAGAGGAGTAACC
GGGCCTTAACTTTTTGCGCTCGTTTTGCTATAATTTTTCTCTATCCACCTCCATCCCACC
CCCACAACACTCTTTACTGGGGGGGTCTTTTGTGTTCCGGATCTCCCCCTCCATGGCTCC
CTTAGCCGAAGTCGGGGGCTTTCTGGGCGGCCTGGAGGGCTTGGGCCAGCAGGTGGGTTC
GCATTTCCTGTTGCCTCCTGCCGGGGAGCGGCCGCCGCTGCTGGGCGAGCGCAGGAGCGC
GGCGGAGCGGAGCGCGCGCGGCGGGCCGGGGGCTGCGCAGCTGGCGCACCTGCACGGCAT
CCTGCGCCGCCGGCAGCTCTATTGCCGCACCGGCTTCCACCTGCAGATCCTGCCCGACGG
CAGCGTGCAGGGCACCCGGCAGGACCACAGCCTCTTCGGTACGTACTAGCATCCCGACCC
CACCCCCATCTGCGCCCCAGCTCGGCTCCTCGTTCCCTCCCCTTGCACCTCCCTCTTTGC
CTGCCAAGGGCGTCATCGCCGCGCGGAGCCCGGAGCTCCCCTGGACCCATCCGGTGCAAG
ACGCAGGCTGGGGCTGAAGGGCTGGCCAGAGCAGCCGCGGGGAGAAATTTTCCTGCTGGT
TTGTCGCCGCAGCCTCTAGCAGGGCAGCAGCTCCAGATGCTGGGGGCGGGAGGAGAAAGG
GTGGGCGCTTCGCAAGCTCC
[SEQ ID NO: 159] - FGF20

FIG 2S

GGAGCTTGCGAAGCGCCCACCCTTTCTCCTCCCGCCCCCAGCATCTGGAGCTGCTGCCCT
GCTAGAGGCTGCGGCGACAAACCAGCAGGAAAATTTCTCCCCGCGGCTGCTCTGGCCAGC
CCTTCAGCCCCAGCCTGCGTCTTGCACCGGATGGGTCCAGGGGAGCTCCGGGCTCCGCGC
GGCGATGACGCCCTTGGCAGGCAAAGAGGGAGGTGCAAGGGGAGGGAACGAGGAGCCGAG
CTGGGGCGCAGATGGGGGTGGGGTCGGGATGCTAGTACGTACCGAAGAGGCTGTGGTCCT
GCCGGGTGCCCTGCACGCTGCCGTCGGGCAGGATCTGCAGGTGGAAGCCGGTGCGGCAAT
AGAGCTGCCGGCGGCGCAGGATGCCGTGCAGGTGCGCCAGCTGCGCAGCCCCCGGCCCGC
CGCGCGCGCTCCGCTCCGCCGCGCTCCTGCGCTCGCCCAGCAGCGGCGGCCGCTCCCCGG
CAGGAGGCAACAGGAAATGCGAACCCACCTGCTGGCCCAAGCCCTCCAGGCCGCCCAGAA
AGCCCCCGACTTCGGCTAAGGGAGCCATGGAGGGGGAGATCCGGAACACAAAAGACCCCC
CCAGTAAAGAGTGTTGTGGGGGTGGGATGGAGGTGGATAGAGAAAAATTATAGCAAAACG
AGCGCAAAAAGTTAAGGCCCGGTTACTCCTCTGAGGTCGCTCCGGAGGGACTTTGCACTG
AAATGGCAGGGAAGCTCTCACTGTCTTGGAGCGATCTTCTCTCCTTGGGTAGGTGGGAGC
CGGCTGCTGGCTCTGCAGAA
[SEQ ID NO: 160] - FGF20

CTTAACCCCCCCATCTCCAGTTATCCCAATGAACCGACCCCGAGGGGGCATTTCCGCTGA
AGTCCGGGGCTGTAAAAAATTAAGTGAGAAGAGCCGCGCTAAAGCCAAGCGTCGTCGTCA
CCCAAGGTACTGCGCTGATGCGCTGCGGGCCGACCAGGTGCTCCCGCCGGGGCGTCTTCT
CCTACGCAGGAAGGGCCACGCCGAGAGAGGCAGGCAACAAGGGCACGGCTGGAGGCCGGA
AGGTCACCCCGTCCCCGGCGGGGCGGGCGCGGCCCAGCCTCACTTCCCGGGCACGTTCGG
GCGGGGCGATTGCAGGGAACGGGGCGGGGAGGCGACAGTCCCCGGCTCCGCCGCGCGCCA
GCCCGCCTTCGCTGCCCGGAGGCGCCGCAGGCCTGGGTTCCCGGACAGCTGAGCCCGAGC
GCCGCCTCCCGAAAGGTGAAGGCGGCCCGGGGAGGCGGGGACGGTGACGGGGGCGGGGGC
CGCGGGCGGTCTCCCGACGGCTGTCGCGGGGCCAGCCCAAAGCCCCCGATCCCCGGTAGC
TGCGCTTCCCGCGCGGGGCGCCGGAGTAGGGCGGGCCAAGCTGGCCTGCGGCCGCGGCGG
GAAGAAGGGCTAGCGAAGCACCCCCGACCGGGCCCAGGCGCCGGACGCCGGGGGGCGCCT
CGCTGCAACTTCTCTTTGGAAGCCCCGACACGAGCCCCGGCCCGCGCGCGCGCTCCCCCA
CGGCCACGCGCGCACCCTGCCGCCCGCACCCCCGCGCGCCCTCCGTCTATTTTTTCCTCT
TCCTTTCATCCTCACACTCTAAAATAGGTCAAGGGGTGGAAGTTACACCTGGTGCAGCCC
TCGGCTCTGATGCAAAAGCAGCTTTTGCCCCTGGCTGCGGGACAGCGCTGTGACTACTCG
CAACGGGAGAGCTGCTGCCAGTCGCCACACCGTGCGGAAAGCGCCGGCGACCGGAGCACT
GACAATGGTCTGCATAGGGGAGCGGAGAGAAGCTTCTGTTGCGCCCTAGATCCGCTGCCT
CGGCGCCCGCCCGCAGGGAGGAGGGGGCGCGACAGGTCGTCTAGCGCGTGCCCCGGAGCC
CGCGCCCGGGTCTGGCCGCCTGGGTGAGTTCCTGCTCGTCCCCTGCCTTTCCAGTAGCCC
GGGGTGGCTGTTTACCTTGCAAACAGCCTTGCAATACGATCAAAACAGGCGAGACAGCCA
TGCAGTAAGGGATTGCGGGATGTGCTTTGGGTGTGAGATTGGATAAATCAGAATTCAGAG
ATAAAGGACATGTCTAGTGCCTTAAGGGTTAAAGTGGATT
[SEQ ID NO: 161] - FLJ36980

FIG 2T

AATCCACTTTAACCCTTAAGGCACTAGACATGTCCTTTATCTCTGAATTCTGATTTATCC
AATCTCACACCCAAAGCACATCCCGCAATCCCTTACTGCATGGCTGTCTCGCCTGTTTTG
ATCGTATTGCAAGGCTGTTTGCAAGGTAAACAGCCACCCCGGGCTACTGGAAAGGCAGGG
GACGAGCAGGAACTCACCCAGGCGGCCAGACCCGGGCGCGGGCTCCGGGGCACGCGCTAG
ACGACCTGTCGCGCCCCCTCCTCCCTGCGGGCGGGCGCCGAGGCAGCGGATCTAGGGCGC
AACAGAAGCTTCTCTCCGCTCCCCTATGCAGACCATTGTCAGTGCTCCGGTCGCCGGCGC
TTTCCGCACGGTGTGGCGACTGGCAGCAGCTCTCCCGTTGCGAGTAGTCACAGCGCTGTC
CCGCAGCCAGGGGCAAAAGCTGCTTTTGCATCAGAGCCGAGGGCTGCACCAGGTGTAACT
TCCACCCCTTGACCTATTTTAGAGTGTGAGGATGAAAGGAAGAGGAAAAAATAGACGGAG
GGCGCGCGGGGGTGCGGGCGGCAGGGTGCGCGCGTGGCCGTGGGGGAGCGCGCGCGCGGG
CCGGGGCTCGTGTCGGGGCTTCCAAAGAGAAGTTGCAGCGAGGCGCCCCCCGGCGTCCGG
CGCCTGGGCCCGGTCGGGGGTGCTTCGCTAGCCCTTCTTCCCGCCGCGGCCGCAGGCCAG
CTTGGCCCGCCCTACTCCGGCGCCCCGCGCGGGAAGCGCAGCTACCGGGGATCGGGGGCT
TTGGGCTGGCCCCGCGACAGCCGTCGGGAGACCGCCCGCGGCCCCCGCCCCCGTCACCGT
CCCCGCCTCCCCGGGCCGCCTTCACCTTTCGGGAGGCGGCGCTCGGGCTCAGCTGTCCGG
GAACCCAGGCCTGCGGCGCCTCCGGGCAGCGAAGGCGGGCTGGCGCGCGGCGGAGCCGGG
GACTGTCGCCTCCCCGCCCCGTTCCCTGCAATCGCCCCGCCCGAACGTGCCCGGGAAGTG
AGGCTGGGCCGCGCCCGCCCCGCCGGGGACGGGGTGACCTTCCGGCCTCCAGCCGTGCCC
TTGTTGCCTGCCTCTCTCGGCGTGGCCCTTCCTGCGTAGGAGAAGACGCCCCGGCGGGAG
CACCTGGTCGGCCCGCAGCGCATCAGCGCAGTACCTTGGGTGACGACGACGCTTGGCTTT
AGCGCGGCTCTTCTCACTTAATTTTTTACAGCCCCGGACTTCAGCGGAAATGCCCCCTCG
GGGTCGGTTCATTGGGATAACTGGAGATGGGGGGGTTAAG
[SEQ ID NO: 162] - FLJ36980

CTAGCATTTACTGGATTCCAGAGTCTTGTTATTTAAGAATGCATCTTAAACGGTACTATC
AAATTCATGTTACGTGCAGCCCAGATTGTTTTGGGCAGCACGAAAAGTTTCTGAGGCGCT
GCGTGTACCCCACCCCAGGACACCGTGTGTGCGCGCCGAGCTGAGTGCGAGGAACGTGGC
GCGAGGGCCGGGGGATGCCGGGCTGCGTGGGTGTGAGCCCTCGCGCGACCGCGACCCCGC
GCCTCTCCCGCTCTCGCCGGAACGTGACCGCAGCCGCACCTCTCCTCCAGCCCTTTCCCA
GCCAGACGCTTCCTTTTAGGTCCTTCTGGGCGTTTATTGTAAATTCTGCGACTAAAACAC
GCCGGTGAGCCCGGCCCACCGACAGATGGATCAATCGCCCCCTTCCCGGCTAGGGGAGGA
GGAACCCCCCAACCCCGGAGCCTAGGGAGCCGGGAGCTGCCTCGGGACGAGCTCCTCGGA
GCCCAGCCGGCTGCGGAGCCCCGGCCCGGGTCGGTCTCGGGGCCCTCCTGCCGGGGTGGG
GTGCGAGCCCCTGCCCGATTCCTCTGGGGCGGTTCAGGCAGGTTTGCCGGCCTCCGAGGA
GGTGGTCAGGGCGCCCTGGCCCAGCAGGCTTCTTCCCGAGCCGGGGGGAGGGGAGACCGG
CTGGGGAAGGGGCATCTCGAAGGGGTGGAGGCCGGGGCGGGCGGGAGGCAAGCGCGCCGC
GGGCGTGAGGGCAAAGTTCCCGAGGTCCGCGCGGAGAGCACACGTGTATGTGCGCGCGGG
GCTAGGCCGGGGCCGGCAGGATGCGTTGGGTTCGGGGGCGCGCGGGGCCGGCGCCGAAGG
GGATAATTCCTTTCCCTGGCACCATCGGGGAGACGCTTTGTCGGCCTCGGCTCCTGGGCG
CAGGGACGCCTTAGCCCACGGAGGGTGGAGCCCCCCTCAGACCCGGGCCACCGGCTGGGG
TTTTTCTAACGCCCTGCCCCCCGAGCCCCCGGATGGCTCGGGCCCCACGGACTCCGCGCC
CTCCAGCCTCAGCTCAGCTCCCCAGGCTTCCCAGACCCAGCGGCGCAGGGGGCGGGGGCA
GGGGCAGTGGGGGTTGGAGGGCGCAGCCGGTCCCCAGGGTGGGGAGAGCTGCGGGGGGAG
GAGGAGGAGGGTGCCGACGCTTGAGTGGGTTCGAGCCCGAGCCGTAGCCGGGGGAGCCAG
TCAGTTTCCGGCCAAGGCAGCAGGTCAGTCCCAGGAAGGGCGGGCGATTGAGCCGAGGGA
GCCGGCGGCTGGGCTCTCCTCTCGGCCCGCGATCCCCGGCGCCGCCGCCGCCGCCACCGC
CACCGCCACCGCCTTCGCCTTGTCGCCGCCGCCGCTGCAGAGCATCGTAGCTCCGCCGCG
CTCCCGCGCCCCGCGCCCCGCGCCGCCAGCCGCCTGGGAGCCCGAGCGCCGAGCCCGGGG
CGGAGGAGAGGGGCGCTGGCGCGAGAGCCCGGGCGAGGGAGCCGCGAAGGGAGAAGGGGG
CGGGCGGAGGGAGGAGCAGGGAGAGTGGGAGAAGGGGGAGGGAGAGAGGAGAGCGAGGGA
GAGCTGGAGAGAGCGAGAGCAAAGAGCGAGCGAGGGAGAGGAGAGAGAGAGAGAGGAGAG
AGAAAGACACACGCACGCAGAGACACACGGTCACTGGAATTCCATTAGAAAAAAGTGAGC
CGAGCAAGGGTTAGCGGGAGAAGATTTTTTTGAATCTTGTCTTCGTCTTGGTGCGAAAGA
AGCGACTCCAGTCTCTCGTCCTCGAAGCTCCGACTGGATTGTTCTTGGGCGCTGACACCC
[SEQ ID NO: 163] - GFRA2

FIG 2U

GGGTGTCAGCGCCCAAGAACAATCCAGTCGGAGCTTCGAGGACGAGAGACTGGAGTCGCT
TCTTTCGCACCAAGACGAAGACAAGATTCAAAAAAATCTTCTCCCGCTAACCCTTGCTCG
GCTCACTTTTTTCTAATGGAATTCCAGTGACCGTGTGTCTCTGCGTGCGTGTGTCTTTCT
CTCTCCTCTCTCTCTCTCTCCTCTCCCTCGCTCGCTCTTTGCTCTCGCTCTCTCCAGCTC
TCCCTCGCTCTCCTCTCTCCCTCCCCCTTCTCCCACTCTCCCTGCTCCTCCCTCCGCCCG
CCCCCTTCTCCCTTCGCGGCTCCCTCGCCCGGGCTCTCGCGCCAGCGCCCCTCTCCTCCG
CCCCGGGCTCGGCGCTCGGGCTCCCAGGCGGCTGGCGGCGCGGGGCGCGGGGCGCGGGAG
CGCGGCGGAGCTACGATGCTCTGCAGCGGCGGCGGCGACAAGGCGAAGGCGGTGGCGGTG
GCGGTGGCGGCGGCGGCGGCGCCGGGGATCGCGGGCCGAGAGGAGAGCCCAGCCGCCGGC
TCCCTCGGCTCAATCGCCCGCCCTTCCTGGGACTGACCTGCTGCCTTGGCCGGAAACTGA
CTGGCTCCCCCGGCTACGGCTCGGGCTCGAACCCACTCAAGCGTCGGCACCCTCCTCCTC
CTCCCCCCGCAGCTCTCCCCACCCTGGGGACCGGCTGCGCCCTCCAACCCCCACTGCCCC
TGCCCCCGCCCCCTGCGCCGCTGGGTCTGGGAAGCCTGGGGAGCTGAGCTGAGGCTGGAG
GGCGCGGAGTCCGTGGGGCCCGAGCCATCCGGGGGCTCGGGGGGCAGGGCGTTAGAAAAA
CCCCAGCCGGTGGCCCGGGTCTGAGGGGGGCTCCACCCTCCGTGGGCTAAGGCGTCCCTG
CGCCCAGGAGCCGAGGCCGACAAAGCGTCTCCCCGATGGTGCCAGGGAAAGGAATTATCC
CCTTCGGCGCCGGCCCCGCGCGCCCCCGAACCCAACGCATCCTGCCGGCCCCGGCCTAGC
CCCGCGCGCACATACACGTGTGCTCTCCGCGCGGACCTCGGGAACTTTGCCCTCACGCCC
GCGGCGCGCTTGCCTCCCGCCCGCCCCGGCCTCCACCCCTTCGAGATGCCCCTTCCCCAG
CCGGTCTCCCCTCCCCCCGGCTCGGGAAGAAGCCTGCTGGGCCAGGGCGCCCTGACCACC
TCCTCGGAGGCCGGCAAACCTGCCTGAACCGCCCCAGAGGAATCGGGCAGGGGCTCGCAC
CCCACCCCGGCAGGAGGGCCCCGAGACCGACCCGGGCCGGGGCTCCGCAGCCGGCTGGGC
TCCGAGGAGCTCGTCCCGAGGCAGCTCCCGGCTCCCTAGGCTCCGGGGTTGGGGGGTTCC
TCCTCCCCTAGCCGGGAAGGGGGCGATTGATCCATCTGTCGGTGGGCCGGGCTCACCGGC
GTGTTTTAGTCGCAGAATTTACAATAAACGCCCAGAAGGACCTAAAAGGAAGCGTCTGGC
TGGGAAAGGGCTGGAGGAGAGGTGCGGCTGCGGTCACGTTCCGGCGAGAGCGGGAGAGGC
GCGGGGTCGCGGTCGCGCGAGGGCTCACACCCACGCAGCCCGGCATCCCCCGGCCCTCGC
GCCACGTTCCTCGCACTCAGCTCGGCGCGCACACACGGTGTCCTGGGGTGGGGTACACGC
AGCGCCTCAGAAACTTTTCGTGCTGCCCAAAACAATCTGGGCTGCACGTAACATGAATTT
GATAGTACCGTTTAAGATGCATTCTTAAATAACAAGACTCTGGAATCCAGTAAATGCTAG
[SEQ ID NO: 164] - GFRA2

AAACAGCATTAGCCTTCTCCCATCAAAAGTCCGGAAGCTGCCCTTCAGTCGTCAAAGTGT
TTGCCTTAATTTGCAATCGTTATGACTTGAGCCAAATGCTTATACCTCATTTGTGTCGTA
TATGTGAAGATACAATTGCAAATCGTTCACGACCTTGAGTCAAGACCTTGAGTTTCCTGA
GGTCAGGAGACCGTTAGGGAATGTGAGTGTCCCAGACGGGCGCTGAGCCCAGCTCGGAGA
CCCACCCCGCCCGTAGCAGCGGCGCGGGCCCCAGAGAGCCCCGCACTCGGCCGCGCCTCA
GTTACGCTGACTCGGCTGTGCCCGCAGTGTCGCGCTGTCGCGTAGCCAGGTGTCGCCGGG
CTGGCGCGGTTATTTATGACTGCGTGGTTGGGCTGGGGGTTCGGGGCCGGGGAGCAGCCG
GGATCCGCCGCCTCTTCCATGATCTTCCCGGGCCGAACCACGGGACCGCTACGCTGAAGG
TGGCGTCGCGGGTCCCCGGGGCCGCGCGAGTGTAGGGGTCGCTCTCGGCCGGCCGCGAAG
CTCGCGGCACCGACTTCTCGCGAGATTTCGGCGACCCCCCCCCCCGCCCCCGCCCCTCCG
TTCTCTGCCCCCTCCCAGCTCTGGTGTGGGCGGCCTCCGCTATGGCTGCGCTGCGAAGGC
TCTTGTGGCCGCCACCCCGGGTGTCTCCTCCACTCTGCGCTCACCAGCCCCTCCTTGGGC
CGTGGGGGCGGCCTGCGGTGACCACCCTGGGCCTTCCTGGCCGGCCCTTCTCCTCCCGAG
AGGATGAGGAGAGGGCTGTGGCGGAGGCGGCATGGAGGCGGCGGCGGCGCTGGGGGGAGC
TGAGCGTGGCGGCGGCGGCCGGCGGGGGGCTGGTCGGCCTGGTATGCTACCAGCTGTACG
GGGACCCCAGGGCCGGCTCGCCGGCGACCGGGCGACCCTCAAAGAGCGCGGCCACGGAGC
CCGAGGACCCGCCCCGCGGCCGGGGGATGCTGCCCATCCCAGTGGCGGCTGCCAAGGAGA
CGGTGAGTGCGCGAGCGCGCGTCACACCTGCGCGGGGGATGTGACCTTCGTGCCGGGTAC
GCAGGACCCTGGAGGCTGTGGGGACGGTGCAAGCGCTGTGGCCGCGGGTGAGGAACTTCC
CGTGAGCGAGGCTGACACCTAGGCCGGACAGCCTAGGATCCGGTCACCCACGTATTGGGA
AGACCAGTGATGCTGTCCCTGATGCATCAGGACCTTAAAGGTGGCTGCAGCTACCAAGTA
TCAATCCAAACCCAAAACCAACACCCCTCCCCCTCTTACA
[SEQ ID NO: 165] - EFHA2

FIG 2V

TGTAAGAGGGGGAGGGGTGTTGGTTTTGGGTTTGGATTGATACTTGGTAGCTGCAGCCAC
CTTTAAGGTCCTGATGCATCAGGGACAGCATCACTGGTCTTCCCAATACGTGGGTGACCG
GATCCTAGGCTGTCCGGCCTAGGTGTCAGCCTCGCTCACGGGAAGTTCCTCACCCGCGGC
CACAGCGCTTGCACCGTCCCCACAGCCTCCAGGGTCCTGCGTACCCGGCACGAAGGTCAC
ATCCCCCGCGCAGGTGTGACGCGCGCTCGCGCACTCACCGTCTCCTTGGCAGCCGCCACT
GGGATGGGCAGCATCCCCCGGCCGCGGGGCGGGTCCTCGGGCTCCGTGGCCGCGCTCTTT
GAGGGTCGCCCGGTCGCCGGCGAGCCGGCCCTGGGGTCCCCGTACAGCTGGTAGCATACC
AGGCCGACCAGCCCCCCGCCGGCCGCCGCCGCCACGCTCAGCTCCCCCCAGCGCCGCCGC
CGCCTCCATGCCGCCTCCGCCACAGCCCTCTCCTCATCCTCTCGGGAGGAGAAGGGCCGG
CCAGGAAGGCCCAGGGTGGTCACCGCAGGCCGCCCCCACGGCCCAAGGAGGGGCTGGTGA
GCGCAGAGTGGAGGAGACACCCGGGGTGGCGGCCACAAGAGCCTTCGCAGCGCAGCCATA
GCGGAGGCCGCCCACACCAGAGCTGGGAGGGGGCAGAGAACGGAGGGGCGGGGGCGGGGG
GGGGGGTCGCCGAAATCTCGCGAGAAGTCGGTGCCGCGAGCTTCGCGGCCGGCCGAGAGC
GACCCCTACACTCGCGCGGCCCCGGGGACCCGCGACGCCACCTTCAGCGTAGCGGTCCCG
TGGTTCGGCCCGGGAAGATCATGGAAGAGGCGGCGGATCCCGGCTGCTCCCCGGCCCCGA
ACCCCCAGCCCAACCACGCAGTCATAAATAACCGCGCCAGCCCGGCGACACCTGGCTACG
CGACAGCGCGACACTGCGGGCACAGCCGAGTCAGCGTAACTGAGGCGCGGCCGAGTGCGG
GGCTCTCTGGGGCCCGCGCCGCTGCTACGGGCGGGGTGGGTCTCCGAGCTGGGCTCAGCG
CCCGTCTGGGACACTCACATTCCCTAACGGTCTCCTGACCTCAGGAAACTCAAGGTCTTG
ACTCAAGGTCGTGAACGATTTGCAATTGTATCTTCACATATACGACACAAATGAGGTATA
AGCATTTGGCTCAAGTCATAACGATTGCAAATTAAGGCAAACACTTTGACGACTGAAGGG
CAGCTTCCGGACTTTTGATGGGAGAAGGCTAATGCTGTTT
[SEQ ID NO: 166] - EFHA2

CCTGGCGCGGACAGGACCCAGAAACAAACCACAGCCCGGGGCGCAGCCGCCAGGGCGAAG
GTTAGTTCCGGTCCCTTCCCCTCCCCTCCCCACTTGGACGCGCTTGCGGAGGATTGCGTT
GACGAGACTCTTATTTATTGTCACCAACCTGTGGTGGAATTTGCAGTTGCACATTGGATC
TGATTCGCCCCGCCCCGAATGACGCCTGCCCGGAGGCAGTGAAAGTACAGCCGCGCCGCC
CCAAGTCAGCCTGGACACATAAATCAGCACGCGGCCGGAGAACCCCGCAATCTCTGCGCC
CACAAAATACACCGACGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAG
ACTATAAGAGCGTTCCCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCG
GGGGCCCGGAAAAGGCACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGCCC
CGGGTCCCCAAGACCCTTGTGCTCGTTGTCGCCGCGGTCCTGCTGTTGGTGAGTCCCCGC
CGCGGTCCCTGGCTGGGGAAGAGCGTGCCTGGCGCCTGGAGAGGGCAGGGAGAGAGGGGG
ACACGGCGGGGGTGCGTGGCCCGGGTCGCCTGCGGCCGGGCATGTCCGGGCAAGACGCAC
CAGTCGTCGGAGTCGGGGGAAGAGATGGGTCCCCGGGTTGGGCAGGAGCGACCTGGGCCG
CCAGGGAACAGAGCGCGCGCTCCACTTGGTGTAAATTCCCGAATCCAGTGGGGGAGGGCG
ACAAGGAGGGAATTCCCGAGTAAGCTGCGTGAAGCCACGGAGAGGTCGTCGGACTTTGAT
TTTGTTTTCTTTCCTTACTTTCTGTTTCTTTCTCTTTTTCTCTTTCTTCCTTTCTTTCCC
TCCCTTCCTTCCTCGCTCAGTTCCTGCCTTAATTTCTTTTTCTTTTGCGCCTTCGAATGA
ATTCCTAAAGGCGCTCATTGCAGATCGCTTTGAACCTGCGGCCGGCGAAGAACTCCCCTG
TGGTCGCTGCGGCCCAGTGGTTCCGTTCCGTGCGCGGGAGTCGTCGCGGGCGCAGCTGGA
GAGGCCCCTTCCCCTCCTTAGCGGCTGCGCCCCTACGCGTGCGGGGCCGCTCATCGCCAA
TGCCATTGTTTGGGGTTCCTTGGGAAAACGAGATTTAGGAGAAGGGAGTTGTGGCACTTG
GGGCCTGACCTGCTTGATAATAGCAGCTGCATTTTGGCCTGGGAAGAGCCTTTCTTGCCA
CCTCTTGGCAAGTATCCGTGATAATGGGGAAGGGACAAAG
[SEQ ID NO: 167] - TNFRSF10B

FIG 2W

CTTTGTCCCTTCCCCATTATCACGGATACTTGCCAAGAGGTGGCAAGAAAGGCTCTTCCC
AGGCCAAAATGCAGCTGCTATTATCAAGCAGGTCAGGCCCCAAGTGCCACAACTCCCTTC
TCCTAAATCTCGTTTTCCCAAGGAACCCCAAACAATGGCATTGGCGATGAGCGGCCCCGC
ACGCGTAGGGGCGCAGCCGCTAAGGAGGGGAAGGGGCCTCTCCAGCTGCGCCCGCGACGA
CTCCCGCGCACGGAACGGAACCACTGGGCCGCAGCGACCACAGGGGAGTTCTTCGCCGGC
CGCAGGTTCAAAGCGATCTGCAATGAGCGCCTTTAGGAATTCATTCGAAGGCGCAAAAGA
AAAAGAAATTAAGGCAGGAACTGAGCGAGGAAGGAAGGGAGGGAAAGAAAGGAAGAAAGA
GAAAAAGAGAAAGAAACAGAAAGTAAGGAAAGAAAACAAAATCAAAGTCCGACGACCTCT
CCGTGGCTTCACGCAGCTTACTCGGGAATTCCCTCCTTGTCGCCCTCCCCCACTGGATTC
GGGAATTTACACCAAGTGGAGCGCGCGCTCTGTTCCCTGGCGGCCCAGGTCGCTCCTGCC
CAACCCGGGGACCCATCTCTTCCCCCGACTCCGACGACTGGTGCGTCTTGCCCGGACATG
CCCGGCCGCAGGCGACCCGGGCCACGCACCCCCGCCGTGTCCCCCTCTCTCCCTGCCCTC
TCCAGGCGCCAGGCACGCTCTTCCCCAGCCAGGGACCGCGGCGGGGACTCACCAACAGCA
GGACCGCGGCGACAACGAGCACAAGGGTCTTGGGGACCCGGGGCCCAGGCCTGGCTCCCC
GCGCCTCCCTGGGTCCTGGGCCGTGCCTTTTCCGGGCCCCCGAAGCGGCCGGGGCGTTCT
GTCCCCGTTGTTCCATGGCGGTAGGGAACGCTCTTATAGTCTCTCAGGCCCGTGGGTTTC
AGCCCTTAAAGTAGATCGGGCATCGTCGGTGTATTTTGTGGGCGCAGAGATTGCGGGGTT
CTCCGGCCGCGTGCTGATTTATGTGTCCAGGCTGACTTGGGGCGGCGCGGCTGTACTTTC
ACTGCCTCCGGGCAGGCGTCATTCGGGGCGGGGCGAATCAGATCCAATGTGCAACTGCAA
ATTCCACCACAGGTTGGTGACAATAAATAAGAGTCTCGTCAACGCAATCCTCCGCAAGCG
CGTCCAAGTGGGGAGGGGAGGGGAAGGGACCGGAACTAACCTTCGCCCTGGCGGCTGCGC
CCCGGGCTGTGGTTTGTTTCTGGGTCCTGTCCGCGCCAGG
[SEQ ID NO: 168] - TNFRSF10B

TGCCCCTTTTCTGAGTGCTTGGAAGTGACTGCTGCAAGTGACAAGTGACCACGCCTTTTC
CCCCGCGGGTATAAATTCAGAGGCGCTGCGCTCCGATTCTGGCAGTGCAGCTGTGGGAAC
CTCTCCACGCGCACGAACTCAGCCAACGATTTCTGATAGATTTTTGGGAGTTTGACCAGA
GATGCAAGGGGTGAAGGAGCGCTTCCTACCGTTAGGGAACTCTGGGGACAGAGCGCCCCG
GCCGCCTGATGGCCGAGGCAGGGTGCGACCCAGGACCCAGGACGGCGTCGGGAACCATAC
CATGGCCCGGATCCCCAAGACCCTAAAGTTCGTCGTCGTCATCGTCGCGGTCCTGCTGCC
AGTGAGTCCCGGCCGCGGTCCCTGGCTGGGGAAGAGCGCACCTGGCGCCGGGAGGGGGCA
GGGAGACGGGGACACGGCAGGGATGCCTGGCCCTGGTCACCTGCGGCCGGGCATGTCCGG
GCAGGACGAACTCGCCGTCGGAGTCAGGGGAAGAACTGGGTCCCCGGGCTGGGCAGGAGG
GACCCGGCCGCGAGGGAGCAGAGAGGCGGTCCCCCTGGCTGCCCCGAGCCCGCGAAGGGA
GGGAAGTTCCAGAATCGAGAGAGGGAGGGAGTCAAGGTGGAACCCATAGAGTGAGCCTCC
TGAAGACACAGAGCGGTTGCCTCTCTCATTAATTAATTAATTAGTTAATAAAATTAACCC
CATGTTTACATTCTTAAACGTGTTCCTTGGAGATCGGTTTAACCAACAGCCAGTGAAAAA
ACTTTTCAGCGCTGTCTTTA
[SEQ ID NO: 169] - TNFRSF10C

TAAAGACAGCGCTGAAAAGTTTTTCACTGGCTGTTGGTTAAACCGATCTCCAAGGAACA
CGTTTAAGAATGTAAACATGGGGTTAATTTTATTAACTAATTAATTAATTAATGAGAGAG
GCAACCGCTCTGTGTCTTCAGGAGGCTCACTCTATGGGTTCCACCTTGACTCCCTCCCTC
TCTCGATTCTGGAACTTCCCTCCCTTCGCGGGCTCGGGGCAGCCAGGGGGACCGCCTCTC
TGCTCCCTCGCGGCCGGGTCCCTCCTGCCCAGCCCGGGGACCCAGTTCTTCCCCTGACTC
CGACGGCGAGTTCGTCCTGCCCGGACATGCCCGGCCGCAGGTGACCAGGGCCAGGCATCC
CTGCCGTGTCCCCGTCTCCCTGCCCCCTCCCGGCGCCAGGTGCGCTCTTCCCCAGCCAGG
GACCGCGGCCGGGACTCACTGGCAGCAGGACCGCGACGATGACGACGACGAACTTTAGGG
TCTTGGGGATCCGGGCCATGGTATGGTTCCCGACGCCGTCCTGGGTCCTGGGTCGCACCC
TGCCTCGGCCATCAGGCGGCCGGGGCGCTCTGTCCCCAGAGTTCCCTAACGGTAGGAAGC
GCTCCTTCACCCCTTGCATCTCTGGTCAAACTCCCAAAAATCTATCAGAAATCGTTGGCT
GAGTTCGTGCGCGTGGAGAGGTTCCCACAGCTGCACTGCCAGAATCGGAGCGCAGCGCCT
CTGAATTTATACCCGCGGGGGAAAAGGCGTGGTCACTTGTCACTTGCAGCAGTCACTTCC
AAGCACTCAGAAAAGGGGCA
[SEQ ID NO: 170] - TNFRSF10C

FIG 2X

GAAATAACTTGAGCCAGGGATCAAACACTAAGATTGGCAGGAAATGAGCAGGAAGAGGTA
GCGGGGTCCCTGACGCCATCTATTCAATTGTTTTTCAGAAGAGGTATCAGCTCTTGAAGG
CTTACTTCTCAATACTGGCTGCGAGAGCAAGAATGGTGTGTAATTTACAAAAGCCGTCAT
TGCTGTAGGTAAGTTGTAGCAAACGACTCGCGCCCGAGCATTCCCGCCCCCGCCTTCGCT
GCGGCCCCGCCCACGACGACCCTGGGGAACTACAAGTCCCGCCATACAGCGGGGAGCGCC
CGGAGCTCGCGCCGGCCCCGCCCCCAGCCCGGTCCCCACCCCCGGCTCCGCCCCCGGCCC
CCTCCCGCCGGGTCAACCCCGAAGAGTCGCCGGTGGCCGCGGCAGACGGAAGCCGAACGA
GTTCCTCGGCGGCTGCAGGATGGGGGACTCCAAAGTGAAAGTGGCGGTGCGGATACGACC
CATGAACCGGCGAGGTGAGAGCCGAGCCCTCCTGGGCCGCCGGGGCGGAGGCGGCAGGTG
CCTGGCGCGCCCTTCCCTCGGCCGCCGTGGGGGGTCCGGCGGCCCCGCCCCTATAGTCAG
CGGCGGGGCGCGAGGAGGGGCCCGGGGACCCTGAAACCCGCTCCCGCGCTGAGACGCCCG
GCTCCCTCTTCTCCCCTCCCTTCCCCCCTGGCCAGCCCCGTCCCTGGCGCCGTCGGGCCC
CTCGTGCCGGCCCCGCTGCCCCTTCCGCCTGCGCCCGCCCCGCCCCTGCGCCCTTTTGCC
CTCTCGTCTCCCCCGGAGGTTCCCGAGGGCGCCCTCGGCCCTCGCGCCCAGCCTCGTCCT
GGCCCCTCAGCCTCGCTCCTTCCCCGCCAGCTGTCATCGTCGCCCCCGCGCGCGGGTCGC
CAGCCCCTGCAGCCCGCCTCGGGACCGCCCGGGACCCCCCGGGACCCCGCGTCTCGCCCG
GGTCGCCCAAGCCTGCACCGCCTTGGCCCGCGGCGGGAAGAAGGGCAGGGGGCCAGGCGG
GTGCCCCGCGGCGAGTTCCTTCCACCTGGGCGTCCTGAGATTGGGGTCAGGTGGAGGAGA
TGCCCTTTTCGTTGTTTTTGGACAGTTGAGAAAGTTTTGGTTTTGCCTGAAGTCTCATTC
ATCATCTCTCAATAAATAGCTAAAGTGCCAAGATTCTTGTGGAATTGTATCTTTCTGACA
TTCTCTTAACTCTGCAGGGAGTGTAGAGAAGGCAGATAAACCGAGTACATTTAAATAATC
TGTAGACCCGGGGAGTGGAGAGAACCCCAAAAGTCAGGGG
[SEQ ID NO: 171] - KIF13B

CCCCTGACTTTTGGGGTTCTCTCCACTCCCCGGGTCTACAGATTATTTAAATGTACTCGG
TTTATCTGCCTTCTCTACACTCCCTGCAGAGTTAAGAGAATGTCAGAAAGATACAATTCC
ACAAGAATCTTGGCACTTTAGCTATTTATTGAGAGATGATGAATGAGACTTCAGGCAAAA
CCAAAACTTTCTCAACTGTCCAAAAACAACGAAAAGGGCATCTCCTCCACCTGACCCCAA
TCTCAGGACGCCCAGGTGGAAGGAACTCGCCGCGGGGCACCCGCCTGGCCCCCTGCCCTT
CTTCCCGCCGCGGGCCAAGGCGGTGCAGGCTTGGGCGACCCGGGCGAGACGCGGGGTCCC
GGGGGGTCCCGGGCGGTCCCGAGGCGGGCTGCAGGGGCTGGCGACCCGCGCGCGGGGGCG
ACGATGACAGCTGGCGGGGAAGGAGCGAGGCTGAGGGGCCAGGACGAGGCTGGGCGCGAG
GGCCGAGGGCGCCCTCGGGAACCTCCGGGGGAGACGAGAGGGCAAAAGGGCGCAGGGGCG
GGGCGGGCGCAGGCGGAAGGGGCAGCGGGGCCGGCACGAGGGGCCCGACGGCGCCAGGGA
CGGGGCTGGCCAGGGGGGAAGGGAGGGGAGAAGAGGGAGCCGGGCGTCTCAGCGCGGGAG
CGGGTTTCAGGGTCCCCGGGCCCCTCCTCGCGCCCCGCCGCTGACTATAGGGGCGGGGCC
GCCGGACCCCCCACGGCGGCCGAGGGAAGGGCGCGCCAGGCACCTGCCGCCTCCGCCCCG
GCGGCCCAGGAGGGCTCGGCTCTCACCTCGCCGGTTCATGGGTCGTATCCGCACCGCCAC
TTTCACTTTGGAGTCCCCCATCCTGCAGCCGCCGAGGAACTCGTTCGGCTTCCGTCTGCC
GCGGCCACCGGCGACTCTTCGGGGTTGACCCGGCGGGAGGGGGCCGGGGGCGGAGCCGGG
GGTGGGGACCGGGCTGGGGGCGGGGCCGGCGCGAGCTCCGGGCGCTCCCCGCTGTATGGC
GGGACTTGTAGTTCCCCAGGGTCGTCGTGGGCGGGGCCGCAGCGAAGGCGGGGGCGGGAA
TGCTCGGGCGCGAGTCGTTTGCTACAACTTACCTACAGCAATGACGGCTTTTGTAAATTA
CACACCATTCTTGCTCTCGCAGCCAGTATTGAGAAGTAAGCCTTCAAGAGCTGATACCTC
TTCTGAAAAACAATTGAATAGATGGCGTCAGGGACCCCGCTACCTCTTCCTGCTCATTTC
CTGCCAATCTTAGTGTTTGATCCCTGGCTCAAGTTATTTC
[SEQ ID NO: 172] - KIF13B

FIG 2Y

ACCCCCTCCTTCCTTCTTTCCCTACCGCCCCACGCGCGACCCGGGGATGGCTCCGTGGCC
TCACGAGAACAGCTCTCTTGCCCCATGGCCGGACCTCCCCACCCTGGCGCCCAATACCGC
CAACACCAGTGGGCTGCCAGGGGTTCCGTGGGAGGCGGCCCTAGCCGGGGCCCTGCTGGC
GCTGGCGGTGCTGGCCACCGTGGGAGGCAACCTGCTGGTCATCGTGGCCATCGCCTGGAC
TCCGAGACTCCAGACCATGACCAACGTGTTCGTGACTTCGCTGGCCGCAGCCGACCTGGT
GATGGGACTCCTGGTGGTGCCGCCGGCGGCCACCTTGGCGCTGACTGGCCACTGGCCGTT
GGGCGCCACTGGCTGCGAGCTGTGGACCTCGGTGGACGTGCTGTGTGTGACCGCCAGCAT
CGAAACCCTGTGCGCCCTGGCCGTGGACCGCTACCTGGCTGTGACCAACCCGCTGCGTTA
CGGCGCACTGGTCACCAAGCGCTGCGCCCGGACAGCTGTGGTCCTGGTGTGGGTCGTGTC
GGCCGCGGTGTCGTTTGCGCCCATCATGAGCCAGTGGTGGCGCGTAGGGGCCGACGCCGA
GGCGCAGCGCTGCCACTCCAACCCGCGCTGCTGTGCCTTCGCCTCCAACATGCCCTACGT
GCTGCTGTCCTCCTCCGTCTCCTTCTACCTTCCTCTTCTCGTGATGCTCTTCGTCTACGC
GCGGGTTTTCGTGGTGGCTACGCGCCAGCTGCGCTTGCTGCGCGGGGAGCTGGGCCGCTT
TCCGCCCGAGGAGTCTCCGCCGGCGCCGTCGCGCTCTCTGGCCCCGGCCCCGGTGGGGAC
GTGCGCTCCGCCCGAAGGGGTGCCCGCCTGCGGCCGGCGGCCCGCGCGCCTCCTGCCTCT
CCGGGAACACCGGGCCCTGTGCACCTTGGGTCTCATCATGGGCACCTTCACTCTCTGCTG
GTTGCCCTTCTTTCTGGCCAACGTGCTGCGCGCCCTGGGGGGCCCCTCTCTAGTCCCGGG
CCCGGCTTTCCTTGCCCTGAACTGGCTAGGTTATGCCAATTCTGCCTTCAACCCGCTCAT
CTACTGCCGCAGCCCGGACTTTCGCAGCGCCTTCCGCCGTCTTCTGTGCCGCTGCGGCCG
TCGCCTGCCTCCGGAGCCCTGCGCCGCCGCCCGCCCGGCCCTCTTCCCCTCGGGCGTTCC
TGCGGCCCGGAGCAGCCCAGCGCAGCCCAGGCTTTGCCAACGGCTCGACGGGTAGGTAAC
CGGGGCAGAGGGACCGGCGGCTCAGGGTCGGGAAGCATGCGATGTGTCCGTGGGTCAACT
TTTTGAGTGTGGAGTTTATTAAGAGAAGGTGGGATGGCTTTGCTTGGAGAGAAAAGGGAA
CGAGGAGTAGCGAACCAAAATGGGACCCAGGGTCCTTTTCTTTCCGGATCCAGTCACTAG
GGTAGAAGCAAAGGAGGGCGAGCGGGCCGTCGTTCCTCACCCAAGGACCCAAGGTGCGCC
ACCGGAAAGCGCTGCGGTGTCCCGAGGACTCTCGCCTCGCCTGGTCGGCT
[SEQ ID NO: 173] - ADRB3

AGCCGACCAGGCGAGGCGAGAGTCCTCGGGACACCGCAGCGCTTTCCGGTGGCGCACCTT
GGGTCCTTGGGTGAGGAACGACGGCCCGCTCGCCCTCCTTTGCTTCTACCCTAGTGACTG
GATCCGGAAAGAAAAGGACCCTGGGTCCCATTTTGGTTCGCTACTCCTCGTTCCCTTTTC
TCTCCAAGCAAAGCCATCCCACCTTCTCTTAATAAACTCCACACTCAAAAAGTTGACCCA
CGGACACATCGCATGCTTCCCGACCCTGAGCCGCCGGTCCCTCTGCCCCGGTTACCTACC
CGTCGAGCCGTTGGCAAAGCCTGGGCTGCGCTGGGCTGCTCCGGGCCGCAGGAACGCCCG
AGGGGAAGAGGGCCGGGCGGGCGGCGGCGCAGGGCTCCGGAGGCAGGCGACGGCCGCAGC
GGCACAGAAGACGGCGGAAGGCGCTGCGAAAGTCCGGGCTGCGGCAGTAGATGAGCGGGT
TGAAGGCAGAATTGGCATAACCTAGCCAGTTCAGGGCAAGGAAAGCCGGGCCCGGGACTA
GAGAGGGGCCCCCCAGGGCGCGCAGCACGTTGGCCAGAAAGAAGGGCAACCAGCAGAGAG
TGAAGGTGCCCATGATGAGACCCAAGGTGCACAGGGCCCGGTGTTCCCGGAGAGGCAGGA
GGCGCGCGGGCCGCCGGCCGCAGGCGGGCACCCCTTCGGGCGGAGCGCACGTCCCCACCG
GGGCCGGGGCCAGAGAGCGCGACGGCGCCGGCGGAGACTCCTCGGGCGGAAAGCGGCCCA
GCTCCCCGCGCAGCAAGCGCAGCTGGCGCGTAGCCACCACGAAAACCCGCGCGTAGACGA
AGAGCATCACGAGAAGAGGAAGGTAGAAGGAGACGGAGGAGGACAGCAGCACGTAGGGCA
TGTTGGAGGCGAAGGCACAGCAGCGCGGGTTGGAGTGGCAGCGCTGCGCCTCGGCGTCGG
CCCCTACGCGCCACCACTGGCTCATGATGGGCGCAAACGACACCGCGGCCGACACGACCC
ACACCAGGACCACAGCTGTCCGGGCGCAGCGCTTGGTGACCAGTGCGCCGTAACGCAGCG
GGTTGGTCACAGCCAGGTAGCGGTCCACGGCCAGGGCGCACAGGGTTTCGATGCTGGCGG
TCACACACAGCACGTCCACCGAGGTCCACAGCTCGCAGCCAGTGGCGCCCAACGGCCAGT
GGCCAGTCAGCGCCAAGGTGGCCGCCGGCGGCACCACCAGGAGTCCCATCACCAGGTCGG
CTGCGGCCAGCGAAGTCACGAACACGTTGGTCATGGTCTGGAGTCTCGGAGTCCAGGCGA
TGGCCACGATGACCAGCAGGTTGCCTCCCACGGTGGCCAGCACCGCCAGCGCCAGCAGGG
CCCCGGCTAGGGCCGCCTCCCACGGAACCCCTGGCAGCCCACTGGTGTTGGCGGTATTGG
GCGCCAGGGTGGGGAGGTCCGGCCATGGGGCAAGAGAGCTGTTCTCGTGAGGCCACGGAG
CCATCCCCGGGTCGCGCGTGGGGCGGTAGGGAAAGAAGGAAGGAGGGGGT
[SEQ ID NO: 174] - ADRB3

FIG 2Z

CGCAGACCCAGCAGGAGAGCGCAACCTAGCATCTTTAAGGTTCGCTTAGCCCTTCCTGTG
CACCTGGAAGGAAGCCTTATCTTAAACTCCCTTCCACCTAGAGTTTATTTTCGCCTGCGT
GCGACAGGGCTTTTGTACTTAAGTGAGTTAAGGAATGAACCCCGAACTCTTCTGGGAAAG
CCACCAACGTTCCCCCCGCACCCCTCCCAGGGTTCCTGACCACGGAGACTCTGCTTGGGG
CACAGGTGTGGGAGTCGCAAACTTTTCTCTGCGCCGTCCTTTTCCGCGTGGAATGGACG
GAGCAGCCCTCCCAGGCGCTGCCTGGCTGCGGAGGGGAGCGGGCAGCGAGAGCCTCGGGT
CTCCGCCTGGGTTCCCGGGTCTCCGGGGCGCTGGCCTCGGTCTCCGCGCAGCGTCCAGCG
ACCCCTGTCGGGGGTTCCCGGCAGCCGCGCCGCCACCCCCCGCCCGGCCAGCGCGGGAGG
AAAAGGGGCTGCGCCCGGGAGCGCCGAGCCCAGGCTCCTCCCGGTGGCGTGTCCGCGCCT
CGGGGTGGGGGTGTGGTGGGGAAGAGGGAGGGGGCGAGGCCAGGGGAGGGTGCGAAGGAG
GCGCCTGCCTCCAACCTGCGGGCGGGAGGTGGGTGGCTGCGGGGCAATTGAAAAAGAGCC
GGCGAGGAGTTCCCCGAAACTTGTTGGAACTCCGGGCTCGCGCGGAGGCCAGGAGCTGAG
CGGCGGCGGCTGCCGGACGATGGGAGCGTGAGCAGGACGGTGATAACCTCTCCCCGATCG
GGTTGCGAGGGCGCCGGGCAGAGGCCAGGACGCGAGCCGCCAGCGGTGGGACCCATCGAC
GACTTCCCGGGGCGACAGGAGCAGCCCCGAGAGCCAGGGCGAGCGCCCGTTCCAGGTGGC
CGGACCGCCCGCCGCGTCCGCGCCGCGCTCCCTGCAGGCAACGGGAGACGCCCCCGCGCA
GCGCGAGCGCCTCAGCGCGGCCGCTCGCTCTCCCCCTCGAGGGACAAACTTTTCCCAAAC
CCGATCCGAGCCCTTGGACCAAACTCGCCTGCGCCGAGAGCCGTCCGCGTAGAGCGCTCC
GTCTCCGGCGAGATGTCCGAGCGCAAAGAAGGCAGAGGCAAAGGGAAGGGCAAGAAGAAG
GAGCGAGGCTCCGGCAAGAAGCCGGAGTCCGCGGCGGGCAGCCAGAGCCCAGGTGGGTGC
GCAGCGCGGCCCGGGCCCCACGATCCTCCTCCTGCTCCTCCTACTCCTCCTCCTCCTCGG
ATGCCGTGGCCTCTCCCTCCCCCTCTCCCTCGCCCGTCCTCTTCGCCCTGCGCTCTGAGC
GCCCGTTGAGTCGCGCGGTGCTTCCCCTCCTGGGGGCCGCCGCTCACCTGGGCGCCGAGT
CCTACCGGGCGCCTACGCCCAGAGCTCAGGGCAAGGGACAGCAGTCCCGGCCGCACCCTC
CCAGAGTCCCGGGAGCGCTTCGCTCCCTGGCACGGCCCCTCCCCAGCGCCTTAGCGGCTG
AGCCCAGCCCGGGAGTGGGACCTGGGCTATAGGAGTCGAGGCTGCGTGCGCGCGTGCCCC
GCGCCATAAGCGCTTTGCACGGGGGCCGTGTGCCCTCTAGCGGGAAACGCTGGAATGGGC
CGCCTGGAGGGAGAGCCGGTCCCCTCGGTGTGCCTGGCAGCGCAGAAGTGGGTGGTCGAG
CAAGAGGCCGCGTGGGAAGTTAGCTTCGGCGTTTTGGGGCACAGGGCAAGCGATGTAGAG
TGCGCGCCGGTTCATCTTGATTCAGTCCTGTGCTACGGAGACTCAAGAGCAGCGGCAGGG
[SEQ ID NO: 175] - NRG1

FIG 2AA

```
CCCTGCCGCTGCTCTTGAGTCTCCGTAGCACAGGACTGAATCAAGATGAACCGGCGCGCA
CTCTACATCGCTTGCCCTGTGCCCCAAAACGCCGAAGCTAACTTCCCACGCGGCCTCTTG
CTCGACCACCCACTTCTGCGCTGCCAGGCACACCGAGGGGACCGGCTCTCCCTCCAGGCG
GCCCATTCCAGCGTTTCCCGCTAGAGGGCACACGGCCCCCGTGCAAAGCGCTTATGGCGC
GGGGCACGCGCGCACGCAGCCTCGACTCCTATAGCCCAGGTCCCACTCCCGGGCTGGGCT
CAGCCGCTAAGGCGCTGGGGAGGGGCCGTGCCAGGGAGCGAAGCGCTCCCGGGACTCTGG
GAGGGTGCGGCCGGGACTGCTGTCCCTTGCCCTGAGCTCTGGGCGTAGGCGCCCGGTAGG
ACTCGGCGCCCAGGTGAGCGGCGGCCCCCAGGAGGGGAAGCACCGCGCGACTCAACGGGC
GCTCAGAGCGCAGGGCGAAGAGGACGGGCGAGGGAGAGGGGGAGGGAGAGGCCACGGCAT
CCGAGGAGGAGGAGGAGTAGGAGGAGCAGGAGGAGGATCGTGGGGCCCGGGCCGCGCTGC
GCACCCACCTGGGCTCTGGCTGCCCGCCGCGGACTCCGGCTTCTTGCCGGAGCCTCGCTC
CTTCTTCTTGCCCTTCCCTTTGCCTCTGCCTTCTTTGCGCTCGGACATCTCGCCGGAGAC
GGAGCGCTCTACGCGGACGGCTCTCGGCGCAGGCGAGTTTGGTCCAAGGGCTCGGATCGG
GTTTGGGAAAAGTTTGTCCCTCGAGGGGGAGAGCGAGCGGCCGCGCTGAGGCGCTCGCGC
TGCGCGGGGGCGTCTCCCGTTGCCTGCAGGGAGCGCGGCGCGGACGCGGCGGGCGGTCCG
GCCACCTGGAACGGGCGCTCGCCCTGGCTCTCGGGGCTGCTCCTGTCGCCCCGGGAAGTC
GTCGATGGGTCCCACCGCTGGCGGCTCGCGTCCTGGCCTCTGCCCGGCGCCCTCGCAACC
CGATCGGGGAGAGGTTATCACCGTCCTGCTCACGCTCCCATCGTCCGGCAGCCGCCGCCG
CTCAGCTCCTGGCCTCCGCGCGAGCCCGGAGTTCCAACAAGTTTCGGGGAACTCCTCGCC
GGCTCTTTTTCAATTGCCCCGCAGCCACCCACCTCCCGCCCGCAGGTTGGAGGCAGGCGC
CTCCTTCGCACCCTCCCCTGGCCTCGCCCCCTCCCTCTTCCCCACCACACCCCCACCCCG
AGGCGCGGACACGCCACCGGGAGGAGCCTGGGCTCGGCGCTCCCGGGCGCAGCCCCTTTT
CCTCCCGCGCTGGCCGGGCGGGGGGTGGCGGCGCGGCTGCCGGGAACCCCCGACAGGGGT
CGCTGGACGCTGCGCGGAGACCGAGGCCAGCGCCCCGGAGACCCGGGAACCCAGGCGGAG
ACCCGAGGCTCTCGCTGCCCGCTCCCCTCCGCAGCCAGGCAGCGCCTGGGAGGGCTGCTC
CGTCCCATTCCACGCGGAAAAGGACGGCGCAGAGAAAAGTTTGCGACTCCCACACCTGTG
CCCCAAGCAGAGTCTCCGTGGTCAGGAACCCTGGGAGGGGTGCGGGGGGAACGTTGGTGG
CTTTCCCAGAAGAGTTCGGGGTTCATTCCTTAACTCACTTAAGTACAAAAGCCCTGTCGC
ACGCAGGCGAAAATAAACTCTAGGTGGAAGGGAGTTTAAGATAAGGCTTCCTTCCAGGTG
CACAGGAAGGGCTAAGCGAACCTTAAAGATGCTAGGTTGCGCTCTCCTGCTGGGTCTGCG
```

[SEQ ID NO: 176] - NRG1

FIG 2BB

GGGAGGGTGGCCTGCAAGGCGGGGCCGGTTGCGGTCAAGTTCAAGTAGGGTCAGAGCAGG
AGAACACTGGCATAAAAAATAGCCACATCCAAGGAAGCAGTGAGGTGTGGGGACCATCTA
TTTCGGTGGGCCTTCCCACCCCCAGGCCGGCCTTCCCATCACGCGTGGGTGTGGGGGCAC
TGCCCCCGCTGCGCGCAGGAACAGCGGGGAGAGCCAGGAGCGGAGCGGCTTCGGGATGCC
AGACTGAGCAGTGGGTTCGTCTGCGGCCACCTCTCAGGGAACAAGCTTCCCCCCGCGGAG
ACTCTGCTTCTTTTAAAAGCCTTCCTGGGTTTAGTCTAGGGCGACAGGACGACCTCCCTT
GGGAAGGGAGAGCCTGCCAGTCCCCCTCCCATTCGCCAGGCGGTGCAGCCCCTCCTCCCG
CCCGGGGCGCGCGCACCTCAGCGTCGCGGGCCTAGCGCCCAGCAGCCGCGCCCCAGGCCG
GGCCTCGGGTTCCGGGAGCCCGCAGGCGCGCGCCCGGCCGGGCGTGTCGGGAGCGCGCGG
CGGCCGGGGGCGGAGCGCAGCCAGGGCTGCGCGGCGCGCCCCGGCTCCCGCCCGCTCCCA
GCCGGGCCCCCCAGCGGTCGGCGGGACGGCTCCCGGCTGCAGTCTGCCCGCCCGCCCCGC
GCGGGGGCCGAGTCGCGAAGCGCGCCTGCGACCCGGCGTCCGGGCGCGCTGGAGAGGACG
CGAGGAGCCATGAGGCGCCAGCCTGCGAAGGTGGCGGCGCTGCTGCTCGGGCTGCTCTTG
GAGGTAGGGGCCGGGGACCGGGTGCTGCCGGAGGCGCGGCGCCCACCATGCTGGCGGCTG
GGGGCGCGCAGTTCCGAGGCGCCCCAGAGGACCTTGCCTGGGAGCGCAGACGGTGGAGCG
ACGGGGAGCCACAGCCCTGCGCGCCTCCCGGAGCTGGGAGGTGCGGGACCCTGGTGACGG
GGAGGCTCCCGCCCCGGTCCGCGCCTTCCGTCGTTCCTTCGGTTTTCGCACCCCGCCCCC
ACCCTGCGGGTGAGCGCGTTTCCCGCGCCGACCGCCTCCGTTAGCTCGGGGTGACCTTTG
TGCACCGTCCGCCCCCTCTCCCCGCCGCAGAGGGCCGAGGATCGGATGGACCCGGGGTTG
GGCGGGGGTGGTCCTCGGGCGCGGCGCAGGCGCGGAGAGCCCGGGGCGCCGGGCAGTTTG
GGGTTAGGAAAGGATGGGTGCCGAGCCGGGGTGAGGGGAGCGGGCGGAGGGGACTGTGGG
GAAGTGTCGCGGGAGTGCCGGGAGTTGTGGAGGTGAGCAGCGGGAGGAGGCGTTCCCGCG
TGTGAAAATGAAGTGCAGCCTTTAGGTGCGGGGAGGAAATTCTGCGGAGAGCCTGGCTGG
GTGGGGGTGCGGAGCCGAAGCCGGCGGGGAACTTGTTGAGCGGCTTCCGGGTGCGAGCGC
CCGTGACCGCATCCCTGGCGGGGACCGCGGCTGCTCCTGGCTGTGAAATTGCATCCTCGG
ATGGGGCCACATACTTCTCACTAAAGCAGGTTCCTTAAAATGCGAACTAG
[SEQ ID NO: 177] - ECOP

CTAGTTCGCATTTTAAGGAACCTGCTTTAGTGAGAAGTATGTGGCCCCATCCGAGGATGC
AATTTCACAGCCAGGAGCAGCCGCGGTCCCCGCCAGGGATGCGGTCACGGGCGCTCGCAC
CCGGAAGCCGCTCAACAAGTTCCCCGCCGGCTTCGGCTCCGCACCCCCACCCAGCCAGGC
TCTCCGCAGAATTTCCTCCCCGCACCTAAAGGCTGCACTTCATTTTCACACGCGGGAACG
CCTCCTCCCGCTGCTCACCTCCACAACTCCCGGCACTCCCGCGACACTTCCCCACAGTCC
CCTCCGCCCGCTCCCCTCACCCCGGCTCGGCACCCATCCTTTCCTAACCCCAAACTGCCC
GGCGCCCCGGGCTCTCCGCGCCTGCGCCGCGCCCGAGGACCACCCCCGCCCAACCCCGGG
TCCATCCGATCCTCGGCCCTCTGCGGCGGGGAGAGGGGGCGGACGGTGCACAAAGGTCAC
CCCGAGCTAACGGAGGCGGTCGGCGCGGGAAACGCGCTCACCCGCAGGGTGGGGGCGGGG
TGCGAAAACCGAAGGAACGACGGAAGGCGCGGACCGGGGCGGGAGCCTCCCCGTCACCAG
GGTCCCGCACCTCCCAGCTCCGGGAGGCGCGCAGGGCTGTGGCTCCCCGTCGCTCCACCG
TCTGCGCTCCCAGGCAAGGTCCTCTGGGGCGCCTCGGAACTGCGCGCCCCCAGCCGCCAG
CATGGTGGGCGCCGCGCCTCCGGCAGCACCCGGTCCCCGGCCCCTACCTCCAAGAGCAGC
CCGAGCAGCAGCGCCGCCACCTTCGCAGGCTGGCGCCTCATGGCTCCTCGCGTCCTCTCC
AGCGCGCCCGGACGCCGGGTCGCAGGCGCGCTTCGCGACTCGGCCCCCGCGCGGGGCGGG
CGGGCAGACTGCAGCCGGGAGCCGTCCCGCCGACCGCTGGGGGGCCCGGCTGGGAGCGGG
CGGGAGCCGGGGCGCGCCGCGCAGCCCTGGCTGCGCTCCGCCCCCGGCCGCCGCGCGCTC
CCGACACGCCCGGCCGGGCGCGCGCCTGCGGGCTCCCGGAACCCGAGGCCCGGCCTGGGG
CGCGGCTGCTGGGCGCTAGGCCCGCGACGCTGAGGTGCGCGCGCCCCGGGCGGGAGGAGG
GGCTGCACCGCCTGGCGAATGGGAGGGGGACTGGCAGGCTCTCCCTTCCCAAGGGAGGTC
GTCCTGTCGCCCTAGACTAAACCCAGGAAGGCTTTTAAAAGAAGCAGAGTCTCCGCGGGG
GGAAGCTTGTTCCCTGAGAGGTGGCCGCAGACGAACCCACTGCTCAGTCTGGCATCCCGA
AGCCGCTCCGCTCCTGGCTCTCCCCGCTGTTCCTGCGCGCAGCGGGGGCAGTGCCCCCAC
ACCCACGCGTGATGGGAAGGCCGGCCTGGGGGTGGGAAGGCCCACCGAAATAGATGGTCC
CCACACCTCACTGCTTCCTTGGATGTGGCTATTTTTTATGCCAGTGTTCTCCTGCTCTGA
CCCTACTTGAACTTGACCGCAACCGGCCCCGCCTTGCAGGCCACCCTCCC
[SEQ ID NO: 178] - ECOP

FIG 2CC

TGCTGGGCAATGCGTGCGTGGTGGCTGCCATCGCCTTGGAGCGCTCCCTGCAGAACGTGG
CCAATTATCTTATTGGCTCTTTGGCGGTCACCGACCTCATGGTGTCGGTGTTGGTGCTGC
CCATGGCCGCGCTGTATCAGGTGCTCAACAAGTGGACACTGGGCCAGGTAACCTGCGACC
TGTTCATCGCCCTCGACGTGCTGTGCTGCACCTCATCCATCTTGCACCTGTGCGCCATCG
CGCTGGACAGGTACTGGGCCATCACGGACCCCATCGACTACGTGAACAAGAGGACGCCCC
GGCGCGCCGCTGCGCTCATCTCGCTCACTTGGCTTATTGGCTTCCTCATCTCTATCCCGC
CCATGCTGGGCTGGCGCACCCCGGAAGACCGCTCGGACCCCGACGCATGCACCATTAGCA
AGGATCATGGCTACACTATCTATTCCACCTTTGGAGCTTTCTACATCCCGCTGCTGCTCA
TGCTGGTTCTCTATGGGCGCATATTCCGAGCTGCGCGCTTCCGCATCCGCAAGACGGTCA
AAAAGGTGGAGAAGACCGGAGCGGACACCCGCCATGGAGCATCTCCCGCCCCGCAGCCCA
AGAAGAGTGTGAATGGAGAGTCGGGGAGCAGGAACTGGAGGCTGGGCGTGGAGAGCAAGG
CTGGGGGTGCTCTGTGCGCCAATGGCGCGGTGAGGCAAGGTGACGATGGCGCCGCCCTGG
AGGTGATCGAGGTGCACCGAGTGGGCAACTCCAAAGAGCACTTGCCTCTGCCCAGCGAGG
CTGGTCCTACCCCTTGTGCC
[SEQ ID NO: 179] - HTR1A

GGCACAAGGGGTAGGACCAGCCTCGCTGGGCAGAGGCAAGTGCTCTTTGGAGTTGCCCAC
TCGGTGCACCTCGATCACCTCCAGGGCGGCGCCATCGTCACCTTGCCTCACCGCGCCATT
GGCGCACAGAGCACCCCCAGCCTTGCTCTCCACGCCCAGCCTCCAGTTCCTGCTCCCCGA
CTCTCCATTCACACTCTTCTTGGGCTGCGGGGCGGGAGATGCTCCATGGCGGGTGTCCGC
TCCGGTCTTCTCCACCTTTTTGACCGTCTTGCGGATGCGGAAGCGCGCAGCTCGGAATAT
GCGCCCATAGAGAACCAGCATGAGCAGCAGCGGGATGTAGAAAGCTCCAAAGGTGGAATA
GATAGTGTAGCCATGATCCTTGCTAATGGTGCATGCGTCGGGGTCCGAGCGGTCTTCCGG
GGTGCGCCAGCCCAGCATGGGCGGGATAGAGATGAGGAAGCCAATAAGCCAAGTGAGCGA
GATGAGCGCAGCGGCGCGCCGGGGCGTCCTCTTGTTCACGTAGTCGATGGGGTCCGTGAT
GGCCCAGTACCTGTCCAGCGCGATGGCGCACAGGTGCAAGATGGATGAGGTGCAGCACAG
CACGTCGAGGGCGATGAACAGGTCGCAGGTTACCTGGCCCAGTGTCCACTTGTTGAGCAC
CTGATACAGCGCGGCCATGGGCAGCACCAACACCGACACCATGAGGTCGGTGACCGCCAA
AGAGCCAATAAGATAATTGGCCACGTTCTGCAGGGAGCGCTCCAAGGCGATGGCAGCCAC
CACGCACGCATTGCCCAGCA
[SEQ ID NO: 180] - HTR1A

TGACGCAAGGTCCAGTCCAGATTGCCAGGCCCGGGGCATGAGAGAGGATCCTTGTAGGTT
TCGGAGGTGGGGGGGCTGCACTCCATTGTTCACTCCGGGCCAATCAGGGTTGGCCCACTT
CCTCCCAGCCAATCTCCCTTCACCCCCAGCCTCCAACCCAACCCACCCCGCCCATCAGCC
CCTGGATCCCCATCACCTCCCCCGCATCCCCGGCAGTTCTGGGGAAGCTTCGTGACGCCA
CAGGTCCCGCCCCCAGCTCCGGCCCGGGGCTAGTGCGTGTTGACGTCATGCTGCGTGCGG
GCCGGTGCGGAATCGCTCCTTCAACTCCGCGGGGCAGTAGGAGTTAGTTAGCAAAGAGCC
GAGGCCGGGCGCGCGACCCTCGTCCTTCTGCCCCTGGCCGCACACTTTGCGCACATCTCT
TTTTCTGCATGGTGGATATTATTTTTCATTATCCTTTTCTGGGTGCTATGGGTGATCATT
CCAAGAGTAAGTATTTCTGTGTGTGTGTGGGGTGGGGTGTGTGTGTATGCTTAATATGCA
AAATTTCTAA
[SEQ ID NO: 181] - ISL2

FIG 2DD

TTAGAAATTTTGCATATTAAGCATACACACACACCCCACCCCACACACACACAGAAATAC
TTACTCTTGGAATGATCACCCATAGCACCCAGAAAAGGATAATGAAAAATAATATCCACC
ATGCAGAAAAAGAGATGTGCGCAAAGTGTGCGGCCAGGGGCAGAAGGACGAGGGTCGCGC
GCCCGGCCTCGGCTCTTTGCTAACTAACTCCTACTGCCCCGCGGAGTTGAAGGAGCGATT
CCGCACCGGCCCGCACGCAGCATGACGTCAACACGCACTAGCCCCGGGCCGGAGCTGGGG
GCGGGACCTGTGGCGTCACGAAGCTTCCCCAGAACTGCCGGGGATGCGGGGGAGGTGATG
GGGATCCAGGGGCTGATGGGCGGGGTGGGTTGGGTTGGAGGCTGGGGGTGAAGGGAGATT
GGCTGGGAGGAAGTGGGCCAACCCTGATTGGCCCGGAGTGAACAATGGAGTGCAGCCCCC
CCACCTCCGAAACCTACAAGGATCCTCTCTCATGCCCCGGGCCTGGCAATCTGGACTGGA
CCTTGCGTCA
[SEQ ID NO: 182] - ISL2

CAGGGAACAGACCCAGTAGTTGGCTTGGATCTCTTAACTCCAGAAAAGGCCGAGTGAGGA
CAAGGGAGACCACAGGGATAATTTCTGTGGCTCTGGTAAGGGGATGACAAGGGAGAAAAA
CTTTCCCACGGTTCCGTCTGGCCCGCGGCGCTTGTCTGCCTGCGCGGGGTCAAAGCCCGG
CGCCGCCCACGCGCGGCTCGGGTGGGAACCCGCAGACGTGGGGCGAGCAGGGCCGCTGGC
TGTGGCGGGCGAGCGCCGGGGCGCCACGTCCGAGGCCGCGGGGTCGGGGCTGCAGGCACA
GCTCGAGCGCTTTCCGCGGGGTTTGGCTCCTGTCGCTTCCCGTCTCGCCGAACCGGCATC
GCCGCCGCCGGAGCCGCAGCGAGTCCTCAGAGCCTGGCTGCTGGCGGCCGGGAGCGCCGG
GACGGGGCGCGAAGCCGGAGGCTCCGGGACGTGGATACAGGTAAAGGCCGGCGGGTCGGA
GTCGGGCGGGGCGCGGCGGCGGCGCCTCTCGGAGGGACCTGGCCTCGGCCGGGCCCTACC
CAGCCGCGGTGGCCCGGGCCCCCACGTTGGCCCAGGCGGGGACGTGCCAAGGGGCTGGGC
TAGGGTTGCCGCTGGCCTGGCCGCCTCTCGCCCGGCGGGCCTCAGGTGACGCGGCCGCGG
CTTAACTTTCGCACCTGAGGCTCTCGGAGCGGCCTCGGGGCGCGCCCACCTGGAGGTTGG
AATTACACAGGGTCGAAAAAGCTGAGTCCTGGAGGCGAGGCGCTGTAGGTGTGGCGGAGG
AGGCCGGGGAAGGTGGGGTGGGTGCCAGGGGTCCAGTACTGAACCCTCTCCAGGTCTGAG
GTGGGGAACTGCGTCTTGTTTAATTTCGGAGCTTGTGGGGACCACACAGCCCCTTCCACG
GCCGATTCCCTCTGCACGGTTCCACTTTCCTTTGTCTAGCCCATTTCAGTATCGGCGTCG
CAGTCGCTTTTGTTGCAGCCTTGGGTCCGGAGTGTACGACTTTCTGCTAGGCAGAGGTCA
TAAGCTCTGAAATCCATCGGGCGGAGGTGG
[SEQ ID NO: 183] - LOC285671

CCACCTCCGCCCGATGGATTTCAGAGCTTATGACCTCTGCCTAGCAGAAAGTCGTACACT
CCGGACCCAAGGCTGCAACAAAAGCGACTGCGACGCCGATACTGAAATGGGCTAGACAAA
GGAAAGTGGAACCGTGCAGAGGGAATCGGCCGTGGAAGGGGCTGTGTGGTCCCCACAAGC
TCCGAAATTAAACAAGACGCAGTTCCCCACCTCAGACCTGGAGAGGGTTCAGTACTGGAC
CCCTGGCACCCACCCCACCTTCCCCGGCCTCCTCCGCCACACCTACAGCGCCTCGCCTCC
AGGACTCAGCTTTTTCGACCCTGTGTAATTCCAACCTCCAGGTGGGCGCGCCCCGAGGCC
GCTCCGAGAGCCTCAGGTGCGAAAGTTAAGCCGCGGCCGCGTCACCTGAGGCCCGCCGGG
CGAGAGGCGGCCAGGCCAGCGGCAACCCTAGCCCAGCCCCTTGGCACGTCCCCGCCTGGG
CCAACGTGGGGGCCCGGGCCACCGCGGCTGGGTAGGGCCCGGCCGAGGCCAGGTCCCTCC
GAGAGGCGCCGCCGCCGCGCCCCGCCCGACTCCGACCCGCCGGCCTTTACCTGTATCCAC
GTCCCGGAGCCTCCGGCTTCGCGCCCCGTCCCGGCGCTCCCGGCCGCCAGCAGCCAGGCT
CTGAGGACTCGCTGCGGCTCCGGCGGCGGCGATGCCGGTTCGGCGAGACGGGAAGCGACA
GGAGCCAAACCCCGCGGAAAGCGCTCGAGCTGTGCCTGCAGCCCCGACCCCGCGGCCTCG
GACGTGGCGCCCCGGCGCTCGCCCGCCACAGCCAGCGGCCCTGCTCGCCCCACGTCTGCG
GGTTCCCACCCGAGCCGCGCGTGGGCGGCGCCGGGCTTTGACCCCGCGCAGGCAGACAAG
CGCCGCGGGCCAGACGGAACCGTGGGAAAGTTTTTCTCCCTTGTCATCCCCTTACCAGAG
CCACAGAAATTATCCCTGTGGTCTCCCTTGTCCTCACTCGGCCTTTTCTGGAGTTAAGAG
ATCCAAGCCAACTACTGGGTCTGTTCCCTG
[SEQ ID NO: 184] - LOC285671

FIG 2EE

GGCAGCAGCCGCTGGCTTCTGCGCCCACTAGGAGCTTCGGATGCCCGAGTTAGGGCTGCG
CCAAGGCGGCCGGAGCAGAGAGGGAGACGGGGACGGGGACAGGCAGGGACAAAGTGCAAG
AGGCAAAACTGGCTGAAAAGCAGAAGTGTAGGAGCCGCCAAGGGGCGGGACGAACAGGTC
CGTGGGCCGGGCGGAGCCAAGGGTGGGGGCCGGGGTCCCTCCAGGTGGCACTCGCGGCGC
TAGTCCCCAGCCTCCTCCCTTCCCCCGGCCCTGATTGGCAGGCGGCCTGCGACCAGCCGC
GAACGCCACAGCGCCCCGGGCGCCCAGGAGAACGCGAACGGCCCCCCGCGGGAGCGGGCG
AGTAGGAGGGGGCGCCGGGCTATATATATAGCGGCTCGGCCTCGGGCGGGCCTGGCGCTC
AGGGAGGCGCGCACTGCTCCTCAGAGTCCCAGCTCCAGCCGCGCGCTTTCCGCCCGGCTC
GCCGCTCCATGCAGCCGGGGTAGAGCCCGGCGCCCGGGGGCCCCGTCGCTTGCCTCCCGC
ACCTCCTCGGTTGCGCACTCCTGCCCGAGGTCGGCCGTGCGCTCCCGCGGGACGCCACAG
GCGCAGCTCTGCCCCCCAGCTTCCCGGGCGCACTGACCGCCTGACCGACGCACGGCCCTC
GGGCCGGGATGTCGGGGCCCGGGACGGCCGCGGTAGCGCTGCTCCCGGCGGTCCTGCTGG
CCTTGCTGGCGCCCTGGGCGGGCCGAGGGGGCGCCGCCGCACCCACTGCACCCAACGGCA
CGCTGGAGGCCGAGCTGGAGCGCCGCTGGGAGAGCCTGGTGGCGCTCTCGTTGGCGCGCC
TGCCGGTGGCAGCGCAGCCCAAGGAGGCGGCCGTCCAGAGCGGCGCCGGCGACTACCTGC
TGGGCATCAAGCGGCTGCGGCGGCTCTACTGCAACGTGGGCATCGGCTTCCACCTCCAGG
CGCTCCCCGACGGCCGCATCGGCGGCGCGCACGCGGACACCCGCGACAGTGAGTGGCGCG
GCCAGGCGCGAAGGGGCGGGGGCGGGGGGCAACGGCCGCCGGGCCAACCCGCTCAGTCAC
ACTCTGAGACCCTCGGCGGGCACCTGCTCGGGGGCCCCGGGAACCGGGGCGGACTCGGGC
TCCGGTCCCTTCTGACGCGGGGCTGGGGACGCAGACACTCTTGGCTCCGGCAGCCCAGCG
CAACCCCTGAGGTCGGGCGCCGCCTCCCGCCTTCAGAAACTCGGGCTCCGAGCGCCGAAT
TCCAGCGCCTTCGCCCGTGGGCACAGGGCGCGCGGTGCAGCCACAGGGGGCCCGAGACAC
GCGCCCCGGCCTGGCCCAGGCTGGGGAACCGCTGGGGTCGGGCTCGCGTCTGAAGGTCCG
GGACTGGGTGCGGCCGCCGGGGGTCCCCTACACAGGCAAGCTAATCTGAGCTAGCGCAGG
CTTGGGCTCCGGAGGCCCTAGAGGGCAGCTTGGGCTCTGGAGGCCCTTGGGGGCGGCTGC
GCCGGGAACCCTGGCCCTTTATCCCCAACCCCACCCCAGAAATAGGGTCCCCGGAGGCGA
ACAAGCCGAGGGGCGGAGTGGGCCAGGGATCACCTGCCCCGCAATGACCTGCGCCCCGCC
CCCAGGCCTGCTGGAGCTCTCGCCCGTGGAGCGGGGCGTGGTGAGCATCTTCGGCGTGGC
CAGCCGGTTCTTCGTGGCCATGAGCAGCAAGGGCAAGCTCTATGGCTCGGTGAGTACCGC
AGGGGTCTGGCTAGGCACCTAGTTGGGAACAGCGGACATGGCTAGCAGGCTCGTGGCTTC
[SEQ ID NO: 185] - FGF4

FIG 2FF

GAAGCCACGAGCCTGCTAGCCATGTCCGCTGTTCCCAACTAGGTGCCTAGCCAGACCCCT
GCGGTACTCACCGAGCCATAGAGCTTGCCCTTGCTGCTCATGGCCACGAAGAACCGGCTG
GCCACGCCGAAGATGCTCACCACGCCCCGCTCCACGGGCGAGAGCTCCAGCAGGCCTGGG
GGCGGGGCGCAGGTCATTGCGGGGCAGGTGATCCCTGGCCCACTCCGCCCCTCGGCTTGT
TCGCCTCCGGGGACCCTATTTCTGGGGTGGGGTTGGGGATAAAGGGCCAGGGTTCCCGGC
GCAGCCGCCCCCAAGGGCCTCCAGAGCCCAAGCTGCCCTCTAGGGCCTCCGGAGCCCAAG
CCTGCGCTAGCTCAGATTAGCTTGCCTGTGTAGGGGACCCCCGGCGGCCGCACCCAGTCC
CGGACCTTCAGACGCGAGCCCGACCCCAGCGGTTCCCCAGCCTGGGCCAGGCCGGGGCGC
GTGTCTCGGGCCCCCTGTGGCTGCACCGCGCGCCCTGTGCCCACGGGCGAAGGCGCTGGA
ATTCGGCGCTCGGAGCCCGAGTTTCTGAAGGCGGGAGGCGGCGCCCGACCTCAGGGGTTG
CGCTGGGCTGCCGGAGCCAAGAGTGTCTGCGTCCCCAGCCCCGCGTCAGAAGGGACCGGA
GCCCGAGTCCGCCCCGGTTCCCGGGGCCCCCGAGCAGGTGCCCGCCGAGGGTCTCAGAGT
GTGACTGAGCGGGTTGGCCCGGCGGCCGTTGCCCCCCGCCCCCGCCCCTTCGCGCCTGGC
CGCGCCACTCACTGTCGCGGGTGTCCGCGTGCGCGCCGCCGATGCGGCCGTCGGGGAGCG
CCTGGAGGTGGAAGCCGATGCCCACGTTGCAGTAGAGCCGCCGCAGCCGCTTGATGCCCA
GCAGGTAGTCGCCGGCGCCGCTCTGGACGGCCGCCTCCTTGGGCTGCGCTGCCACCGGCA
GGCGCGCCAACGAGAGCGCCACCAGGCTCTCCCAGCGGCGCTCCAGCTCGGCCTCCAGCG
TGCCGTTGGGTGCAGTGGGTGCGGCGGCGCCCCCTCGGCCCGCCCAGGGCGCCAGCAAGG
CCAGCAGGACCGCCGGGAGCAGCGCTACCGCGGCCGTCCCGGGCCCCGACATCCCGGCCC
GAGGGCCGTGCGTCGGTCAGGCGGTCAGTGCGCCCGGGAAGCTGGGGGGCAGAGCTGCGC
CTGTGGCGTCCCGCGGGAGCGCACGGCCGACCTCGGGCAGGAGTGCGCAACCGAGGAGGT
GCGGGAGGCAAGCGACGGGGCCCCCGGGCGCCGGGCTCTACCCCGGCTGCATGGAGCGGC
GAGCCGGGCGGAAAGCGCGCGGCTGGAGCTGGGACTCTGAGGAGCAGTGCGCGCCTCCCT
GAGCGCCAGGCCCGCCCGAGGCCGAGCCGCTATATATATAGCCCGGCGCCCCCTCCTACT
CGCCCGCTCCCGCGGGGGGCCGTTCGCGTTCTCCTGGGCGCCCGGGGCGCTGTGGCGTTC
GCGGCTGGTCGCAGGCCGCCTGCCAATCAGGGCCGGGGGAAGGGAGGAGGCTGGGGACTA
GCGCCGCGAGTGCCACCTGGAGGGACCCCGGCCCCCACCCTTGGCTCCGCCCGGCCCACG
GACCTGTTCGTCCCGCCCCTTGGCGGCTCCTACACTTCTGCTTTTCAGCCAGTTTTGCCT
CTTGCACTTTGTCCCTGCCTGTCCCCGTCCCCGTCTCCCTCTCTGCTCCGGCCGCCTTGG
CGCAGCCCTAACTCGGGCATCCGAAGCTCCTAGTGGGCGCAGAAGCCAGCGGCTGCTGCC
[SEQ ID NO: 186] - FGF4

TGAGGTGAGGGGCCGGAGGAGCAAGGGACAAGAGGAGCAGAGGACAGGTGATGGAAATCC
TGCAGCTTTAGGCTCCATTCTGCCATCTACATCCCAGCGCAGGGTGAAGCCTGAGAGCCC
AAATGGCCAACTCCACAGGGCTGAACGCCTCAGAAGTCGCAGGCTCGTTGGGGTTGATCC
TGGCAGCTGTCGTGGAGGTGGGGGCACTGCTGGGCAACGGCGCGCTGCTGGTCGTGGTGC
TGCGCACGCCGGGACTGCGCGACGCGCTCTACCTGGCGCACCTGTGCGTCGTGGACCTGC
TGGCGGCCGCCTCCATCATGCCGCTGGGCCTGCTGGCCGCACCGCCGCCCGGGCTGGGCC
GCGTGCGCCTGGGCCCCGCGCCATGCCGCGCCGCTCGCTTCCTCTCCGCCGCTCTGCTGC
CGGCCTGCACGCTCGGGGTGGCCGCACTTGGCCTGGCACGCTACCGCCTCATCGTGCACC
CGCTGCGGCCAGGCTCGCGGCCGCCGCCTGTGCTCGTGCTCACCGCCGTGTGGGCCGCGG
CGGGACTGCTGGGCGCGCTCTCCCTGCTCGGCACGCCGCCCGCACCGCCCCCTGCTCCTG
CTCGCTGCTCGGTCCTGGCTGGGGGCCTCGGGCCCTTCCGGCCGCTCTGGGCCCTGCTGG
CCTTCGCGCTGCCCGCCCTCCTGCTGCTCGGCGCCTACGGCGGCATCTTCGTGGTGGCGC
GTCGCGCTGCCCTGAGGCCCCCACGGCCGGCGCGCGGGTCCCGACTCCACTCGGACTCTC
TGGATAGCCGCCTTTCCATCTTGCCGCCGCTCCGGCCTCGCCTGCCCGGGGGCAAGGCGG
CCCTGGCCCCAGCGCTGGCCGTGGGCCAATTTGCAGCCTGCTGGCTGCCTTATGGCTGCG
CGTGCCTGGCGCCCGCAGCGCGGGCCGCGGAAGCCGAAGCGGCTGTCACCTGGGTCGCCT
ACTCGGCCTTCGCGGCTCACCCCTTCCTGTACGGGCTGCTGCAGCGCCCCGTGCGCTTGG
CACTGGGCCGCCTCTCTCGCCGTGCACTGCCTGGACCTGTGCGGGCCTGCACTCCGCAAG
CCTGGCACCCGCGGGCACTCTTGCAATGCCTCCAGAGACCCCCAGAGGGCCCTGCCGTAG
GCCCTTCTGAGGCTCCAGAACAGACCCCCGAGTTGGCAGGAGGGCGGAGCCCCGCATACC
AGGGGCCACCTGAGAGTTCTCTCTCCTGAGCAGGAGAAAGGAGGGTGGTTTCCGTGGGGG
CTCATCCAACCCCTGCACAGGTCACAGCAGGTGCCCTGCT
[SEQ ID NO: 187] - GPR62

FIG 2GG

AGCAGGGCACCTGCTGTGACCTGTGCAGGGGTTGGATGAGCCCCCACGGAAACCACCCTC
CTTTCTCCTGCTCAGGAGAGAGAACTCTCAGGTGGCCCCTGGTATGCGGGGCTCCGCCCT
CCTGCCAACTCGGGGGTCTGTTCTGGAGCCTCAGAAGGGCCTACGGCAGGGCCCTCTGGG
GGTCTCTGGAGGCATTGCAAGAGTGCCCGCGGGTGCCAGGCTTGCGGAGTGCAGGCCCGC
ACAGGTCCAGGCAGTGCACGGCGAGAGAGGCGGCCCAGTGCCAAGCGCACGGGGCGCTGC
AGCAGCCCGTACAGGAAGGGGTGAGCCGCGAAGGCCGAGTAGGCGACCCAGGTGACAGCC
GCTTCGGCTTCCGCGGCCCGCGCTGCGGGCGCCAGGCACGCGCAGCCATAAGGCAGCCAG
CAGGCTGCAAATTGGCCCACGGCCAGCGCTGGGGCCAGGGCCGCCTTGCCCCCGGGCAGG
CGAGGCCGGAGCGGCGGCAAGATGGAAAGGCGGCTATCCAGAGAGTCCGAGTGGAGTCGG
GACCCGCGCGCCGGCCGTGGGGGCCTCAGGGCAGCGCGACGCGCCACCACGAAGATGCCG
CCGTAGGCGCCGAGCAGCAGGAGGGCGGGCAGCGCGAAGGCCAGCAGGGCCCAGAGCGGC
CGGAAGGGCCCGAGGCCCCCAGCCAGGACCGAGCAGCGAGCAGGAGCAGGGGGCGGTGCG
GGCGGCGTGCCGAGCAGGGAGAGCGCGCCCAGCAGTCCCGCCGCGGCCCACACGGCGGTG
AGCACGAGCACAGGCGGCGGCCGCGAGCCTGGCCGCAGCGGGTGCACGATGAGGCGGTAG
CGTGCCAGGCCAAGTGCGGCCACCCCGAGCGTGCAGGCCGGCAGCAGAGCGGCGGAGAGG
AAGCGAGCGGCGCGGCATGGCGCGGGGCCCAGGCGCACGCGGCCCAGCCCGGGCGGCGGT
GCGGCCAGCAGGCCCAGCGGCATGATGGAGGCGGCCGCCAGCAGGTCCACGACGCACAGG
TGCGCCAGGTAGAGCGCGTCGCGCAGTCCCGGCGTGCGCAGCACCACGACCAGCAGCGCG
CCGTTGCCCAGCAGTGCCCCCACCTCCACGACAGCTGCCAGGATCAACCCCAACGAGCCT
GCGACTTCTGAGGCGTTCAGCCCTGTGGAGTTGGCCATTTGGGCTCTCAGGCTTCACCCT
GCGCTGGGATGTAGATGGCAGAATGGAGCCTAAAGCTGCAGGATTTCCATCACCTGTCCT
CTGCTCCTCTTGTCCCTTGCTCCTCCGGCCCCTCACCTCA
[SEQ ID NO: 188] - GPR62

CCGCGACCTTCGAGAACCCGCATGCTGTTCTCCACCAGGTCTCTCAGTCCTCCCTGCCCC
AATCCCCATGCCCGCCTCCGCGACCCTGTGATGCCTCCCTTCTTGCACAGGAGCAGTGAC
CTCAGCACTTACTTAATCCTCTCCCGGCGCCGAGCTCAGTTGGAGAGGCTAGGGGTGGTA
GTGACTGGCAGGAGGCCGGGGCGGGGGGAACCCCCAAGCCCGGCGTCTGGGGCTGCGGGT
CCGACCCGAGATCCGCCCTCCCTGCAAGCCCCGAGCCGCTGGCCAGGCCCGCTACTGCGC
ACCAGCCGCATCCGCGAGCGCTGGCTCTGCCGGCCTGAGCTAGGGTGGGTAGGGCCGGGA
CCCACGGCGGAGGTGGGGCCGGGCCGAGCAGCCTCGGGGGATCCCCGAAGCTACAGCGCC
TTGCCTCCCTGCACGCTCCGCGCCCCCGGCCTCCGATTGGCTGTCGGGCCTAGAGCCCGC
CCAGAATTGGACCGTTCGCTTGTCGCTCGGGTCTGGCTCCACCCCCAGAGGGAGCCTAGA
ACCTGGTCGCAGTTTTTAGAGACTACCCTCACCCCGTGGCCTGCGCCGAAGTTGGGCGGA
GGACAGTGGGTGGCCAGGCCCTTCCGGGCCAGAACTCGGGACCCCTGCCAGCTACCCGTG
CCAGGACAGACTCAAGCCCCCAAAACGCGGATGGATGTACAGAGGAGACTTGGGGAGAGC
ACTGGACTGGGAGTCCTTGGGCCTGCACTGAACTCTGGCTGACTTTGTGACCTTGAAGAA
ACTGCTTTTCCCTTCCTGAA
[SEQ ID NO: 189] - HEMK1

TTCAGGAAGGGAAAAGCAGTTTCTTCAAGGTCACAAAGTCAGCCAGAGTTCAGTGCAGGC
CCAAGGACTCCCAGTCCAGTGCTCTCCCCAAGTCTCCTCTGTACATCCATCCGCGTTTTG
GGGGCTTGAGTCTGTCCTGGCACGGGTAGCTGGCAGGGGTCCCGAGTTCTGGCCCGGAAG
GGCCTGGCCACCCACTGTCCTCCGCCCAACTTCGGCGCAGGCCACGGGGTGAGGGTAGTC
TCTAAAAACTGCGACCAGGTTCTAGGCTCCCTCTGGGGGTGGAGCCAGACCCGAGCGACA
AGCGAACGGTCCAATTCTGGGCGGGCTCTAGGCCCGACAGCCAATCGGAGGCCGGGGGCG
CGGAGCGTGCAGGGAGGCAAGGCGCTGTAGCTTCGGGGATCCCCCGAGGCTGCTCGGCCC
GGCCCCACCTCCGCCGTGGGTCCCGGCCCTACCCACCCTAGCTCAGGCCGGCAGAGCCAG
CGCTCGCGGATGCGGCTGGTGCGCAGTAGCGGGCCTGGCCAGCGGCTCGGGGCTTGCAGG
GAGGGCGGATCTCGGGTCGGACCCGCAGCCCCAGACGCCGGGCTTGGGGGTTCCCCCCGC
CCCGGCCTCCTGCCAGTCACTACCACCCCTAGCCTCTCCAACTGAGCTCGGCGCCGGGAG
AGGATTAAGTAAGTGCTGAGGTCACTGCTCCTGTGCAAGAAGGGAGGCATCACAGGGTCG
CGGAGGCGGGCATGGGGATTGGGGCAGGGAGGACTGAGAGACCTGGTGGAGAACAGCATG
CGGGTTCTCGAAGGTCGCGG
[SEQ ID NO: 190] - HEMK1

FIG 2HH

CTGCAGCAGGACGTAAGCACAGTCATCGCTGCAAACTGCAAACTCGTAAGCACAGTCATC
GCTGCAAACTGCAAACTCGTGCTCCGAGCGCTGCCCTCCCCTGTGGAGCGGAGGAGGGGA
GGCCTGGGGCCGCGGCGGTGTGCGCCCCGCTCTGACCGCAGAGCCCCCTTCCCGAGGAAA
GCGGCTGGCCCGGTCCCGGCTGGTGATCACGCGGGGCCCCTGTCTGCTTGGTGCGCAGGT
GAGGGTCTGCCCTTCCGCTGCGCCCCGGACAGCCTGGAGGTGAGCACGCGCTGGGCCCTG
GACCGCGAGCAGCGGGAGAAGTACGAGCTGGTGGCCGTGTGCACCGTGCACGCCGGCGCG
CGCGAGGAGGTGGTGATGGTGCCCTTCCCGGTGACCGTGTACGACGAGGACGACTCGGCG
CCCACCTTCCCCGCGGGCGTCGACACCGCCAGCGCCGTGGTGGAGTTCAAGCGGAAGGAG
GTGCTTGTCCGCGCGTGCTGTGGTCTACCCAGTGTCTGTCTCCGGCCACAGTTCGTTTCT
CGGTCGGTTTAGTGTCCGTGTAGCCACCCAACCGTGTGGCCGACCATTCGCGCTTTCATT
TGTCCTTCGCCTCCGTCTGCGCCGTCTGTCCTAGGGGGAGGGGAAGGGGGAGTCCTGCCA
GCACCCAGCTGGGCCTTGCCTCGGGAGGCAAGGACCAGGACGAGGCCCGAGGGCTCGCGT
CTGGGGCATACTTGTGCCGCTGCAGGCGGGCGCGGCGCGCTGCCCGGGCGGGGAGCATCT
GCCGGGAGGGCACTCCCTCCCACCAGCAGTTAGCCCCCAACGGGAGGGCCCTTGAGTGAC
CACGAGCAGAGCCGGGGATTGGAGAAGGACGGGAAGGCGGATCACCTCCGGCGCCGCCCG
CCCCGCCCTTCTCCGGCTCGCGCTGGTGGAGCGCGACCGCCACCTGCTGGGCCTCGGCCT
TCCTGCAGCCGGCCCACCCAGCAGGGGCCGTGGGAGAGTGGGCGTGGGGACTGAGGTAGG
TAGTACGTTGCCTTGTTCCGCTTCTCTGGG
[SEQ ID NO: 191] - RET

CCCAGAGAAGCGGAACAAGGCAACGTACTACCTACCTCAGTCCCCACGCCCACTCTCCCA
CGGCCCCTGCTGGGTGGGCCGGCTGCAGGAAGGCCGAGGCCCAGCAGGTGGCGGTCGCGC
TCCACCAGCGCGAGCCGGAGAAGGGCGGGGCGGGCGGCGCCGGAGGTGATCCGCCTTCCC
GTCCTTCTCCAATCCCCGGCTCTGCTCGTGGTCACTCAAGGGCCCTCCCGTTGGGGGCTA
ACTGCTGGTGGGAGGGAGTGCCCTCCCGGCAGATGCTCCCCGCCCGGGCAGCGCGCCGCG
CCCGCCTGCAGCGGCACAAGTATGCCCCAGACGCGAGCCCTCGGGCCTCGTCCTGGTCCT
TGCCTCCCGAGGCAAGGCCCAGCTGGGTGCTGGCAGGACTCCCCCTTCCCCTCCCCCTAG
GACAGACGGCGCAGACGGAGGCGAAGGACAAATGAAAGCGCGAATGGTCGGCCACACGGT
TGGGTGGCTACACGGACACTAAACCGACCGAGAAACGAACTGTGGCCGGAGACAGACACT
GGGTAGACCACAGCACGCGCGGACAAGCACCTCCTTCCGCTTGAACTCCACCACGGCGCT
GGCGGTGTCGACGCCCGCGGGGAAGGTGGGCGCCGAGTCGTCCTCGTCGTACACGGTCAC
CGGGAAGGGCACCATCACCACCTCCTCGCGCGCGCCGGCGTGCACGGTGCACACGGCCAC
CAGCTCGTACTTCTCCCGCTGCTCGCGGTCCAGGGCCCAGCGCGTGCTCACCTCCAGGCT
GTCCGGGGCGCAGCGGAAGGGCAGACCCTCACCTGCGCACCAAGCAGACAGGGGCCCCGC
GTGATCACCAGCCGGGACCGGGCCAGCCGCTTTCCTCGGGAAGGGGGCTCTGCGGTCAGA
GCGGGGCGCACACCGCCGCGGCCCCAGGCCTCCCCTCCTCCGCTCCACAGGGGAGGGCAG
CGCTCGGAGCACGAGTTTGCAGTTTGCAGCGATGACTGTGCTTACGAGTTTGCAGTTTGC
AGCGATGACTGTGCTTACGTCCTGCTGCAG
[SEQ ID NO: 192] - RET

GCGCCGACGGGGGCGGGTGGTAGGGGATGTACGGGTGTGTATATGCAGAGGTATGCCAGG
CTCTGCCCCTTAAAGTTTGGGGGCCGGCGGAGGCGGCGCCGTGGCCGGGAGAAAGTGTCT
CTCATTTAGGAGGGTTTGCAGGTCCAGAGTAAAGTCACTGAAGAGTGGAAGCGAGGAAGG
AACAGGATGATTAGACCTCAGCTGCGGACCGCGGGGCTGGGACGATGCCTCCTGCCGGGG
CTGCTGCTGCTCCTGGTGCCCGTCCTCTGGGCCGGGGCTGAAAAGCTACATACCCAGCCC
TCCTGCCCCGCGGTCTGCCAGCCCACGCGCTGCCCCGCGCTGCCCACCTGCGCGCTGGGG
ACCACGCCGGTGTTCGACCTGTGCCGCTGTTGCCGCGTCTGCCCCGCGGCCGAGCGTGAA
GTCTGCGGCGGGGCGCAGGGCCAACCGTGCGCCCCGGGGCTGCAGTGCCTCCAGCCGCTG
CGCCCCGGGTTCCCCAGCACCTGCGGTTGCCCGACGCTGGGAGGGGCCGTGTGCGGCAGC
GACAGGCGCACCTACCCCAGCATGTGCGCGCTCCGGGCCGAAAACCGCGCCGCGCGCCGC
CTGGGCAAGGTCCCGGCCGTGCCTGTGCAGTGGGGGAACTGCGGGGATACAGGTGAGCCG
CGGGGGCGCGCGCCCTCGGAACACTTTCTAACTCTGGAGGAGCGTAAAGGAACAAGACCT
CACTGAGACCGCACAGTTCGCGCCTGGTCCTCCTGCGTCATTTGCCTCCTGGATTCGACA
CCTCTGTGTTCCTGATTTCC
[SEQ ID NO: 193] - HTRA4

FIG 2II

GGAAATCAGGAACACAGAGGTGTCGAATCCAGGAGGCAAATGACGCAGGAGGACCAGGCG
CGAACTGTGCGGTCTCAGTGAGGTCTTGTTCCTTTACGCTCCTCCAGAGTTAGAAAGTGT
TCCGAGGGCGCGCGCCCCCGCGGCTCACCTGTATCCCCGCAGTTCCCCCACTGCACAGGC
ACGGCCGGGACCTTGCCCAGGCGGCGCGCGGCGCGGTTTTCGGCCCGGAGCGCGCACATG
CTGGGGTAGGTGCGCCTGTCGCTGCCGCACACGGCCCCTCCCAGCGTCGGGCAACCGCAG
GTGCTGGGGAACCCGGGGCGCAGCGGCTGGAGGCACTGCAGCCCCGGGGCGCACGGTTGG
CCCTGCGCCCCGCCGCAGACTTCACGCTCGGCCGCGGGGCAGACGCGGCAACAGCGGCAC
AGGTCGAACACCGGCGTGGTCCCCAGCGCGCAGGTGGGCAGCGCGGGGCAGCGCGTGGGC
TGGCAGACCGCGGGGCAGGAGGGCTGGGTATGTAGCTTTTCAGCCCCGGCCCAGAGGACG
GGCACCAGGAGCAGCAGCAGCCCCGGCAGGAGGCATCGTCCCAGCCCCGCGGTCCGCAGC
TGAGGTCTAATCATCCTGTTCCTTCCTCGCTTCCACTCTTCAGTGACTTTACTCTGGACC
TGCAAACCCTCCTAAATGAGAGACACTTTCTCCCGGCCACGGCGCCGCCTCCGCCGGCCC
CCAAACTTTAAGGGGCAGAGCCTGGCATACCTCTGCATATACACACCCGTACATCCCCTA
CCACCCGCCCCCGTCGGCGC
[SEQ ID NO: 194] - HTRA4

TTGTCTTCTCCCTTCCGACCTCCCGTGGCCCCAGCGCGGCCAGCTCACAGTAGGTGCTCG
GGCAGCGTTTCTTCAGGGACCTAGACGGCCTGGAGAGGAAGGGCCCCAGCCCAGCCGCCC
GGGCCTCTCACCTGGCTCTCGGGGCGCCCGGCTCGCACTTCCTCCCGCCGCCCCGCCCCT
TCCACATTCCTGCCCCGCCGGGCCTGCCCCGCGCAGTCTGGGTCTCTGCGCCGCAGCCGC
CCGCCCGCCCGCTCAGCGCCCGGCCCCGGGATGACGGCGGCCCAGGCCGCGGGTGAGGAG
GCGCCACCAGGCGTGCGGTCCGTCAAGGTGGTCCTGGTGGGCGACGGCGGCTGCGGGAAG
ACGTCGCTGCTGATGGTCTTCGCCGATGGGGCCTTCCCCGAGGTGAGTGCCCCGCGCCTC
CGCCTCGCCCGGTTCCGCTCGCGCGCCCGGGTGTACAGGTCCGTGCCGGAGCGGCCCAGG
CTGTGCGCCTAACCCGGCCTCCGAGGGGTGTCCCAGCGGGGCCTGGGGTCCAGGGCAGAG
TTCTTCCGCCCCAGCCATTGGGAATGAAGGCCTCAGTGATGTTATCTGTAAAGCCGGAGG
AATGGCATCCACCGGGGAGAGGTGTCACAAGGACTGAGTGAGGCGACCTGGGTGCACACA
AGATCCTAAGACAGCACTTGGCCACACAATTCCGCTGAGGGCCTGAGAGCTTGGAAGCCA
GACTGCCGAGGTTCAAATTATGGCTTTGCCTCTTATAGCTGTGTGCCCTTGGGTAAGTCC
CCTAACCCTGCTGTGCCTGTG
[SEQ ID NO: 195] - RHOD

ATTGAGAGAGAGGGAGGGCGAAAGGAAGGAAGGGGAGCCAGAGGTGGGAGTGGAAGAGGC
AGCCTCGCCTGGGGCTGATTGGCTCCCGAGGCCAGGGCTCTCCAAGCGGTTTATAAGAGT
TGGGGCTGCCGGGCGCCCTGCCCGCTCGCCCGCGCGCCCCAGGACCCAAAGCCGGGCTCC
AAGTCGGCGCCCCACGTCGAGGCTCCGCCGCAGCCTCCGGAGTTGGCCGCAGACAAGAAG
GGGAGGGAGCGGGAGAGGGAGGAGAGCTCCGAAGCGAGAGGGCCGAGCGCCATGCGCCGC
GCCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGGCGGCGGCCCCGGA
GCCCCGCACGAGGGCCCCCTGCACGCCCCGCCGCCGCCTGCGCCGCACCAGCCCCCTGCC
GCCTCCCGCTCCATGTTCGTGGCCCTCCTGGGGCTGGGGCTGGGCCAGGTTGTCTGCAGC
GTCGCCCTGTTCTTCTATTTCAGAGCGCAGGTGAGTGGCCACCTTCCCAGGGGATCGCGG
CTGAGAGCGCCCATCTCCTTCCCCCGCACTTGGAAACTGAGTCTGGCGGCAGGGCTGGGC
CACCCAGAGCTTGCATATTCCGGAAGGGAAAGTGACTCCAGAAGGGAGAGAGGAAGTGTT
GAGTTTGGGGACAACCTGGCGCAGGGCTGTCGGGCGCACCCTGCTCTCTCTCCGCCCACG
CACCCCAGCTTCTCGGTGCTCTGGGGGCGGACTCCCCTGGCCGGACGATGGGTTTGAATC
TCACCCCGTCCCTTCGCTGGGAAACAACACTGGCCTCTCACCTTTTCTGGTAGTGATTGC
ATACTTTTTCTCCCTGTCATTTCTCACTTGAAGTTAAGAATCAACTTCTGTTCACGTAGG
AAAAAAGATGAGCGCCTTCACTTGGGCATCTACCTTTCCCTTCCCGCCCACCACCCGGCG
GGTTTCGGTTCCTGCGCCTGGCTGCTCTGCAGGTGTGCTGGGGCCACGGTGCTGGAGGGC
TGCGCGGAGCGGGAGGTCGCGGTGCTCGTGCCCAGGTCGCCCAATGGGTGGGCAGAATGA
CACGGCGCGACCAGAGAGGCGCGGGCTCGGGATGGGGGCTCTGCGGCTGTGGCGCTGTCC
TGTGGGGGTGAAGGAAGAGGGACAGCCCCACGTGCCTGCTAGGGATGTGGGCGGAGGAAG
GAAGCGAGGTGAGTGTGATGGCACAGTGTTACTACAGTCTAGCAAATAACCAACCTTCGG
AAAGATGAAGAGGTTTTTTGCACGACGGCTAGGAACTGCAG
[SEQ ID NO: 196] - TNFSF11

FIG 2JJ

GCAATTTATAGATGAGAGCGTGGACGGCAGAGAGCATTGTGTATGTTGAAGTCTCTGCGATATGGGGT
GTCCCTGCTGCCCCGCTCCAGCCTTTCACTTCTGACCTCCTTCCTCTGGCTCTTACGCTACAGGATCC
AAAACTACTCGGAAGACTTGCCGCGGGCGGTGATTGACGACGCCTTTGCCCGCGCCTTCGCACTGTGG
AGCGCGGTGACGCCGCTCACCTTCACTCGCGTGTACAGCCGGGACGCAGACATCGTCATCCAGTTTGG
TGTCGCGGGTGAGAACGTGAGGAGGGAAAATCCAAGAGACCTGGGCGGGGTCAGGGAAGGGAGGACCA
CGGAGAGCGTGGAGGCAGCAGTGGCCCCGGCTTCCTCTTGCCTGCCCGCGCTGCCCTGGCTTATACGG
CCCCTCCTGCCAGACAGTGCACAGGGCCAGGGCGCCAGGCTGGGAGAGCTTCGCGCAGGCGGGATTTC
AGCCCGCACTTATTTCGGAGCCCTTGCCTTGGGCAGCGCACAATCTGCGCAGCAGTACTCGGCTAACC
CTCTTCCTCTCGACCTGTTTCTTCAGAGCACGGAGACGGGTATCCCTTCGACGGGAAGGACGGGCTCC
TGGCACACGCCTTTCCTCCTGGCCCCGGCATTCAGGGAGACGCCCATTTCGACGATGACGAGTTGTGG
TCCCTGGGCAAGGGCGTCGGTGAGATTCTGAGTCCTCCTGGCCCCTGATTCCCTTCATTCTCTCCCAC
TCATCACCCGCCGCCCTAACTCCGGTCCCCCCTCCTCCTGCAGTGGTTCCAACTCGGTTTGGAAACGC
AGATGGCGCGGCCTGCCACTTCCCCTTCATCTTCGAGGGCCGCTCCTACTCTGCCTGCACCACCGACG
GTCGCTCCGACGGCTTGCCCTGGTGCAGTACCACGGCCAACTACGACACCGACGACCGGTTTGGCTTC
TGCCCCAGCGAGAGTGAGTGAGGGGGCTCGCCGAGGGCTGGGGGCGCCCACCACCCTTGATGGTCCTG
GGTTCTAATTCCAGCTCTGCCACTAGTGCTGTGTGGCCTGCAATTCACCCTCCCGCACTCTGGGCCCA
ATTTCTCATCTGAGAAATGATGAGAGATGGGATGAACTGCAGACCATCCATGGGTCAAAGAACAGGA
CACACTTGGGGGTTATAATGTGCTGTCTCCGCCTTCTCCCCCTTTCCCACATCCTCCTCGCCCCAGGA
CTCTACACCCAGGACGGCAATGCTGATGGGAAACCCTGCCAGTTTCCATTCATCTTCCAAGGCCAATC
CTACTCCGCCTGCACCACGGACGGTCGCTCCGACGGCTACCGCTGGTGCGCCACCACCGCCAACTACG
ACCGGGACAAGCTCTTCGGCTTCTGCCCGACCCGAGGTACCTCCACCCTGTCTACCAGGTTCAGCCCC
GCCCTCTCATCATGTATTGGCCCCCAAAACGCGGCTCTTCCCTCCCATCAGTTTGTCTTTCCACTCTC
ATTGGTCCTCAGGACGACCGTGACTCCGCCCACCTACACCACATTTCCACCACTATCCCTGACTTCCA
ATGGCCCCGCCCCAGCCACTAAGGTTCGGCCTTTTCTGCCCAGCTGGCCGCCTCTTCCTTGGTCTGGT
GTCCCAGGCACCGCCCACGGGTCTAGCCTCTTCTCAGGAGTGCTCTACAGCGCCCCCTAGGCCACCAA
GATTGTTTAGCTCCCTGTCGGGTCGGCCCCTGACTCCTTATTGGACTCATCCATCTGGCTCATCCAAG
GCCTTGGGTCTCTCCAGCTGACTCGACGGTGATGGGGGGCAACTCGGCGGGGGAGCTGTGCGTCTTCC
CCTTCACTTTCCTGGGTAAGGAGTACTCGACCTGTACCAGCGAGGGCCGCGGAGATGGGCGCCTCTGG
TGCGCTACCACCTCGAACTTTGACAGCGACAAGAAGTGGGGCTTCTGCCCGGACCAAGGTAGGCGTGG
TCCCGCGGCTCCGGGGCTGGGGTTCCCGGCAGTGGTGGTGGTGGGGTGGCCAGGGCTGGGGGCTCGGC
CCGGCGCTCACGTCTCAGGCTCCCTCTCCCTCCAGGATACAGTTTGTTCCTCGTGGCGGCGCATGAGT
TCGGCCACGCGCTGGGCTTAGATCATTCCTCAGTGCCGGAGGCGCTCATGTACCCTATGTACCGCTTC
ACTGAGGGGCCCCCCTTGCATAAGGACGACGTGAATGGCATCCGGCACCTCTATGGTGAGGCAGGGGC
AGGGATGGGAGGAGGAGGGGAAAGGGCGTGGCTGTGCCACAGTACCAAAGAATTGGGGGTTGGGGATC
GGGGGAGGAACGGGGCGTGCAGGAGAGGTGGGACCTCAACGTCTGTCTGGAAGCAGAGCCTGGGCCCA
GTCGCTGCCATGTCAGTGCTTAGAGGTGGTGATAAAGAGACTCTAGAGAGAGATAGGTGTGACTTCAA
AAGCCAGTCTACTCTGGGCATGGTGGCTCACGCCTCTAATCCCAGGGCTTTGGGAGACCCAAGGCGGG
AGGATTGCTTAAGCCCAGGAGTTCCAGACCAGCCTCGGCAACATAGCCAGACTCCCATCTCTACAAAA
AATAAATGAGCAAGGCGTGAAGGCACATGTCTGTAGTCCTAGCTACTCTGGAGGCTGAGGTGGGAGGA
TCTCTTGAGCCCAGGAGTTCGAGGCTGTAGTGAGCTATGATTGCACCACTGCATTCCATCCTGGGCCA
TAGAGGATGTCGCTTAAAACGAAAAAGAAGAAGAAGAAAGTCCTGTGGTTTGGGAAGGGAGGCTGAGT
GAGGAGGGGCCTGTGTGCCAGAGGAGGCTTCACTGAGAAGCTTAGGGGAGCAGATGTTCTAGGGGTAC
AGAGGTATGCAGGAATAGGAAGAGTCTCACCCCGTGTCTCTTTTTAGGTCCTCGCCCTGAACCTGAGC
CACGGCCTCCAACCACCACCACACCGCAGCCCACGGCTCCCCCGACGGTCTGCCCCACCGGACCCCCC
ACTGTCCACCCCTCAGAGCGCCCCACAGCTGGCCCCACAGGTCCCCCCTCAGCTGGCCCCACAGGTCC
CCCCACTGCTGGCCCTTCTACGGCCACTACTGTGCCTTTGAGTCCGGTGGACGATGCCTGCAACGTGA
ACATCTTCGACGCCATCGCGGAGATTGGGAACCAGCTGTATTTGTTCAAGGATGGGTGAGGAGGCGGG
GTTGTGTGGATGCGGGAGGGGGCTTTGCGGAGGGGCTGCCCGTCCCTTCCCGCCCACTGGCCCTGTGT
CCAAGGCTTAGAGCCCGTCCTTTCCCTCCTCGCTTTCTCAGGAAGTACTGGCGATTCTCTGAGGGCAG
GGGGAGCCGGCCGCAGGGCCCCTTCCTTATCGCCGACAAGTGGCCCGCGCTGCCCCGCAAGCTGGACT
CGGTCTTTGAGGAGCGGCTCTCCAAGAAGCTTTTCTTCTTCTCTGGTTAGTTACCTACTTTCCCTCCC
CCGCCCGGTCAATCCCCATCAGTCAAGGAGGCTCAAGAGACCATCGATAACCCACGAAACGTCTTGTG
CGTTTTAGAAAAATACGCCCCCTGGCGGACGCAGTTTAGCAAACGTAGGGGCGGCTGAGTTTCTGCCC
CCTCCTCTCCACGCCCTCGCGTCGCTCTACCCAGCGCCTCTGCCCCTGGGTTGCAGGGACTGCGGGCA
CGCGGGCTAGGAAAGGCCTCGCCGGAATCTCCCTCCTCGCGTTCTAGGAGTACGTGCTCCCTCTGCGC
CCCCAAACCGACGTGACCCTCCTCCCCTGCAGGGCGCCAGGTGTGGGTGTACACAGGCGCGTCGGTGC
TGGGCCCGAGGCGTCTGGACAAGCTGGGCCTGGGAGCCGACGTGGCCCAGGTGACCGGGGCCCTCCGG
AGTGGCAGGGGGAAGATGCTGCTGTTCAGCGGGCGGCGCCTCTGGAGGTGAGCGCCGCCGCGGCCGCC
GGCAGGGGGAGCCCGGGCGCCGTCGGTCCGTCCGCTAGCCGGCTCAGCACCTGTCTCCTCCGCGCCTG
CCCGCAGGTTCGACGTGAAGGCGCAGATGGTGGATCCCCGGAGCGCCAGCGAGGTGGACCGGATGTTC
CCCGGGGTGCCTTTGGACACGCACGACGTCTTCCAGTACCGAGGTGAGGGCTGAGGAGGATCCCTTCG
TGAGACACCACACTAAGCTCCTCTTAGTGAGTGGTCAAATTCTGAGCGAGGAAGAAAAAGCCCTTGGA
AATGGAAACAAATGCCCCAGCACAGACAAGATCCCAGCAGAGGCAGAGGCCTTCTCCAGGTCATTTAG
GAAGTCAGGGATGCAAC
[SEQ ID NO: 197] - MMP9

FIG 2KK

CAGGAACTTTCGAGATGAGGTGCCTTTCCCAAGGTGACACTAAGTGGAGGAGCCCAGCCA
GAGTCCAGGGGTCCTTACACAACCTTCGGTGGTCTCTCTTTACCTGTGAAGCTGCAGCCT
GCTTCCCAGCTCGGGGGCGTGTACAGGAGACTGGACCTGGGGCAGCCTCAGAATGCCTGG
CTGCCTGGAGCTCTCCTCGCGTGTCCAGGCGGCCTGCTTGGTCTCCCTCCTCTCCCCTCT
TAGGTGCCGGGGCGGGCACCCGGTGCAGGGTGGGCACGGCGCCTGCCACCAGCCTCAGGC
GCTGGGAGAAGCGCAGGTTCTTCTGGATAACCGAAGAGACGTCAAAACAGGCTGGGGCAA
AGTGGTCAGAGCAGATGACCGAGCGGTCATTGCCTCCGTACCAGTCGGCGCGGCAACCCC
GCACGAAGCGGTCCCAGAGCAGCCGCACGGCCCGGTCCTTGGGAAAGCGGAACAGCGACT
TCCCAGACTTGGTGGTGTTGCCGCAGTGGGCGGCCACACAACGGGCCGGCATGGCGGCCG
TCTTCGGTGCGCGGGAGCCGGGTTCCCTGGACCTTCGCCCTTGGGCACGCTCCTCGCAGC
GGCCTCGGCGAGGCAAGTCCTCCCCTCCTCACCTGTCCACTCCGGGTCGGGATTGTTTCC
TTCCCTACCTCTGGTCACCGGAAGTGGCGATCTGGGGCCCCCAATGGGAGGGCTCTTTGA
TATCTTCCTCCTCCTCCTCCCTGCGCTGCTCCCCAGGAGCCAGTGGACACAAGCAGAGGG
ATACAAATTTCGCGCGGGCAG
[SEQ ID NO: 198] - LRRC49

MATERIALS AND METHOD FOR ASSAYING FOR METHYLATION OF CPG ISLANDS ASSOCIATED WITH GENES IN THE EVALUATION OF CANCER

CROSS-REFERENCE TO RELATED APPLICATIONS

This patent application is a divisional of U.S. patent application Ser. No. 12/115,674, filed on May 6, 2008, now abandoned, which is a continuation of International Patent Application No. PCT/US2006/060685, filed Nov. 8, 2006, designating the United States, which claims the benefit of U.S. Provisional Patent Application No. 60/734,577, filed Nov. 8, 2005, which are incorporated by reference herein in their entireties.

INCORPORATION-BY-REFERENCE OF MATERIAL SUBMITTED ELECTRONICALLY

Incorporated by reference in its entirety herein is a computer-readable nucleotide/amino acid sequence listing submitted concurrently herewith and identified as follows: One 214,875 Byte ASCII (Text) file named "702375_ST25.TXT," created on May 2, 2008.

BACKGROUND OF THE INVENTION

Phosphate linked cytosine-guanine (CpG) dinucleotides are statistically underrepresented in the genomes of higher eukaryotes, including mammals. The dinucleotide is reportedly found at only 5-10% of its predicted frequency. The majority of CpG dinucleotides that do remain in the human genome are normally located within repetitive sequences that are characterized by low gene expression levels and exhibit methylation at the cytosine residues.

CpG islands, on the other hand, represent genomic sequences that contain clusters of CpG dinucleotide. CpG islands may be associated with the promoter region or 5' end of coding sequences or may be present within introns or in genomic regions that are not known to be associated with coding sequences. They may be unmethylated or methylated in normal tissues and the methylation pattern may be used to control tissue specific expression and the expression of imprinted genes. Methylation of CpG islands within promoter regions can result in the downregulation or silencing of the associated gene. An increase in methylation of normally unmethylated islands is observed in aging tissues even as the overall methylcytosine content of the DNA is reduced. The aberrant methylation pattern is more pronounced in cancer cells with increased methylation or hypermethylation detected in various cancer tissues. CpG islands may be methylated to varying densities within the same tissue. Thus, aberrant methylation of cytosines within CpG islands can be a primary epigenetic event that acts to suppress the expression of genes involved in critical cellular processes, such as DNA damage repair, hormone response, cell-cycle control, and tumor-cell adhesion/metastasis, leading to tumor initiation, progression and metastasis (Li et al., *Biochim. Biophys. Acta,* 1704: 87-102 (2004)). It has been proposed that a unique profile of promoter hypermethylation exists for each human cancer in which some gene changes are shared and other gene changes are cancer-type specific (Esteller et al., *Cancer Res.,* 61: 3225-3229 (2001)). Given that aberrant methylation represents new information not normally present in genomic DNA and that aberrant methylation is a common DNA modification and affects a large number of genomic targets, it is feasible to develop diagnostic and prognostic tests based on information obtained from multiple target CpGs. Such tests may be based on CpGs that are aberrantly hypermethylated or hypomethylated in the diseased tissues. They may also be based on changes in methylation density in CpG islands as long as the changes corrolate with the presence of cancer.

Prostate cancer, for example, which is the most common malignancy and the second leading cause of death among men in the U.S. (Li et al. (2004), supra), has been found to be associated with the methylation of CpG islands in the promoters of over 30 genes, in particular the CpG island of the glutathione S-transferase P1 (GSTP1) gene. GSTP1 methylation has been detected in over 50% of DNA recovered from urine and plasma of prostate cancer patients (Goessl et al., *Ann. N.Y. Acad. Sci.,* 945: 51-58 (2001); Cairns et al., *Clin. Cancer Res.,* 7: 2727-2730 (2001); Jeronimo et al., *Urology,* 60: 1131-1135 (2002); and Gonzalgo et al., *Clin. Cancer Res.,* 9: 2673-2677 (2003)). However, if diagnosis of prostate cancer relied solely on the detection of the methylation of the CpG island in the GSTP1 gene, the theoretical limit of the sensitivity of such a test would only be approximately 90%. GSTP1 is also methylated in prostatic intraepithelial lesions (PIN) which may lead to a false positive diagnosis. Some CpG islands are methylated in prostate cancer and other diseases of the prostate, such as benign prostatic hyperplasia (BPH). They may even exhibit some degree of methylation in normal aging prostates. Such markers may not be suitable individually for prostate cancer diagnosis. Therefore, a panel of markers is required to achieve the sensitivity and specificity needed for a clinical test.

The prostate-specific antigen or PSA test continues to be widely used in the early detection of prostate cancer. While the PSA test has resulted in the majority of prostate cancer cases being diagnosed in asymptomatic men (Mettlin et al., *Cancer,* 83(8): 1679-1684 (1998a); Mettlin et al., *Cancer,* 82(2): 249-251 (1998b); Humphrey et al., *J. Urol.,* 155: 816-820 (1996); and Grossfeld et al., *Epidemiol. Rev.,* 23(1): 173-180 (2001)), the PSA test suffers from poor specificity, which can be as low as 33% when a PSA cut-off level of 2.6 ng/ml is used (Thompson et al., *N. Engl. J. Med.,* 350: 2239-2246 (2004)), even though the sensitivity can be as high as 83%. The poor specificity of the PSA test is a direct result of increased secretion of PSA in other diseases of the prostate, such as BPH and prostatitis. Thus, an elevated PSA level indicates the need for additional screening in the form of needle biopsy. Ultimately, the results of needle biopsies lead to the diagnoses of prostate cancer.

Over 1 million needle biopsies of prostates are performed each year at a cost of about $1,500 each and much discomfort to the patient. However, less than 200,000 of these result in a diagnosis of prostate cancer. Therefore, the majority of needle biopsies are being performed needlessly.

In view of the above, there is a need for non-invasive methods of diagnosing and prognosticating cancer, such as prostate cancer, that reduce the cost and suffering associated with currently available cancer screening methods. It is an object of the invention to provide materials and methods for non-invasive diagnosis and prognosis of cancer, such as prostate cancer. This and other objects and advantages, as well as additional inventive features, will become apparent from the detailed description provided herein.

BRIEF SUMMARY OF THE INVENTION

The invention provides materials and methods for evaluating cancer. Methods of evaluating can include methods of diagnosing and prognosticating cancer as well as methods of assessing the efficacy of cancer treatment. Generally, the methods provided involve assaying for methylation of CpG islands associated with specific genes. The invention also provides pairs of isolated or purified primers that can be used in the methods of the invention, for example, to amplify and/or detect the methylation state of the CpG islands associated with specific genes. The invention also provides kits comprising one or more pairs of primers useful in the disclosed methods.

The invention provides methods of diagnosing cancer by assaying for one or more methylated CpG islands that are indicative of cancer. Generally, the method comprises providing a biological sample from a subject in need of cancer diagnosis and assaying the sample for methylation of one or more CpG islands associated with at least one gene selected from the group consisting of: neuregulin cell-surface ligand (NRG1), adrenergic B3 receptor (ADRB3), glycosylphosphatidyl-inositol cell-surface receptor (GFRA2), kinesin family member 13B (KIF13B), RET proto-oncogene (RET), G-protein-coupled protein receptor 147 (GPR147), neurogenin 3 transcription factor (NEUROG3), paladin (predicted protein tyrosine phosphatase) (PALD), methyltransferase family member 1 (HEMK1), fibroblast growth factor 4 oncogene (FGF4), 5-hydroxytryptamine (serotonin) receptor 1A (HTR1A), ring finger protein 180 (LOG 285671 or RNF180), EGFR-co-amplified and overexpressed (DKFZP564K0822 or ECOP), zinc finger protein 596 (ZNF596), similar to 7 transmembrane helix receptor (LOC441320), L-threonine dehydrogenase (TDH), hypothetical protein FLJ36980 (FLJ36980), fibroblast growth factor receptor 20 (FGF20), EF-hand domain family member 2A (LOC286097 or EFHA2), N-acylsphingosine amidohydrolase (acid ceraminase) 1 (ASAH1), nodal homolog (TGF-β signaling pathway) (NODAL), hypothetical protein similar to zinc finger protein 532 (LOC399783), transcription factor LIM homeodomain (ISL2) Kinesin family member C2 (KIFC2), chromosome 20 open reading frame 23 (Kinesin-like motor protein) (C20orf23), GDNF family receptor alpha 1 (GFRA1), Glutathione peroxidase 7 (GPX7), Dickkopf homolog 2 (DKK2), netrin 1 (NTN1), matrix metallopeptidase 9 (MMP9), tumor necrosis factor superfamily member 11 (TNFSF11), ras homolog gene family member D (RHOD), and leucine rich repeat containing 49 (LRRC49).

The invention also provides a method of diagnosing prostate cancer in a male mammal by assaying for one or more methylated CpG islands that are indicative of prostate cancer. The method can include providing a biological sample from a subject in need of cancer diagnosis and assaying the sample for methylation of a CpG island associated with at least one gene selected from the group consisting of: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, HTR1A, RNF180, ECOP, ZNF596, LOC441320, TDH, FLJ36980, EFHA2, ASAH1, NODAL, LOC399783, ISL2, MMP9, TNFSF11, RHOD, LRRC49, Kinesin family member C2 (KIFC2), chromosome 20 open reading frame 23 (Kinesin-like motor protein) (C20orf23), GDNF family receptor alpha 1 (GFRA1), Glutathione peroxidase 7 (GPX7), Dickkopf homolog 2 (DKK2), netrin 1 (NTN1), Ras association (Ra1GDS/AF-6) domain family 5 (RASSF5), and HtrA serine peptidase 4 (HTRA4). Optionally, the method of diagnosing prostate cancer can also include assaying for methylation of one or more CpG island associated with at least one gene that is known to be methylated in prostate cancer but is known not to be detectably methylated or is methylated at a lower level (e.g., about 50% or less, about 40% or less, 30% or less, about 20% or less, or about 10% or less) in BPH.

The invention also provides methods of prognosticating cancer by assaying for the methylation of one or more genes that are indicative of the grade or stage of the cancer, and/or the length of disease-free survival following treatment for cancer. Generally, the method comprises providing a biological sample from a subject in need of cancer prognosis and assaying the sample for methylation of a CpG island associated with at least one gene selected from the group consisting of: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, HTR1A, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, FLJ36980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, ISL2, KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, MMP9, TNFSF11, RHOD and LRRC49.

Further provided by the invention is a method of prognosticating prostate cancer in a male mammal by assaying for one or more methylated CpG islands that are indicative of the grade or stage of prostate cancer, and/or the length of disease-free survival following treatment of prostate cancer. The method comprises providing a biological sample from the male mammal and assaying the sample for methylation of a CpG island associated with at least one of the following genes: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, GPR62, HTR1A, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, FLJ36980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, ISL2, KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, RASSF5, HTRA4, MMP9, TNFSF11, RHOD or LRRC49. Optionally, the method of prognosticating prostate cancer can also include assaying the biological sample for methylation of a CpG island associated with at least one gene that is known to be methylated in prostate cancer but is known not to be detectably methylated or is methylated at a lower level (e.g., about 50% or less, about 40% or less, 30% or less, about 20% or less, or about 10% or less) in BPH. Methylation of the CpG islands associated with the genes is indicative of the grade or stage of the cancer, and/or the length of disease-free survival following treatment.

Furthermore, the invention provides methods of assessing the efficacy of treatment of cancer by assaying for the reduced methylation of CpG islands that indicates efficacy of treatment. Generally, the method comprises providing a first and a second biological sample from a subject in need of assessing the efficacy of treatment of cancer and assaying the samples for a change in methylation level of a CpG island associated with at least one gene selected from the group consisting of: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, HTR1A, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, FLJ36980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, ISL2, KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, MMP9, TNFSF11, RHOD and LRRC49. The first biological sample is taken before the second biological sample, and the second biological sample is taken during or after a course of treatment. A decrease or absence of methylation of the assayed one or more CpG islands in the second sample (i.e., following the course of treatment) indicates that the treatment is effective. Alternatively, the maintenance or increase of methylation in the assayed CpG islands in the second sample can indicate a reduction or absence of treatment efficacy.

Also provided is a method of assessing the efficacy of treatment of prostate cancer in a male mammal by assaying biological samples, which are taken from the male mammal periodically during the course of treatment, for methylation of a CpG island and wherein a decrease or absence of methylation of the CpG islands following the course of treatment indicates that the treatment is effective. The method comprises (a) providing a first and a second biological sample from a subject undergoing a course of cancer treatment, wherein the first sample is taken at an earlier time than the second sample, and the second sample is taken during or following a course of treatment and (b) assaying the samples for methylation of a CpG island associated with at least one gene selected from the group consisting of: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, HTR1A, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, FLJ36980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, ISL2, KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, RASSF5, HTRA4, MMP9, TNFSF11, RHOD and LRRC49. Optionally, this method can also include assaying the biological sample for methylation of a CpG island associated with at least one gene that is known to be methylated in prostate cancer but is known not to be detectably methylated or is methylated at a lower level (e.g. about 50% or less, about 40% or less, 30% or less, about 20% or less, or about 10% or less in BPH.

In preferred embodiments, the aforementioned methods of diagnosing, prognosticating and assessing the efficacy of treatment of cancer can further include assaying the biological sample for methylation of multiple CpG islands, for example, CpG islands associated with two, three, four, five, six, seven, eight, nine, ten, eleven, or more genes.

Additionally, the invention provides a terminator-coupled linear amplification method of determining the methylation status of a CpG island. Generally, the method includes providing a DNA sample for terminator-coupled linear amplification and then incubating the DNA sample under deaminating conditions to thereby produce a deaminated DNA sample. Optionally, the deaminated DNA sample can be purified. The deaminated sample is used as template to amplify a target sequence or target sequences that include one or more CpG islands or portions of one or more CpG islands thereby producing one or more amplified target sequences. Optionally, the one or more amplified target sequences are purified. One or more sequences in the amplified target sequences are linearly amplified in the presence of a primer and a dideoxynucleotide to generate one or more fragments of different lengths, wherein each length corresponds to the distance in bases from the 5' end of the primer to the position where the dideoxynucleotide is incorporated. Optionally, the one or more fragments is purified. The one or more fragments are analyzed to determine their lengths. The lengths of the fragments can be used to determine the methylation status of methylated cytosines within the one or more amplified target sequences.

The invention also provides pairs of primers suitable for amplifying a CpG-island associated with genes described herein. Primers can include isolated or purified nucleic acid molecules suitable for amplifying a CpG island containing target sequence. Target sequences can include genomic sequence that has been fully methylated and fully deaminated such as those in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 53, and SEQ ID NO: 54.

Exemplary primer pairs include SEQ ID NOs: 55 and 56, SEQ ID NOs: 57 and 58, SEQ ID NOs: 59 and 60, SEQ ID NOs: 61 AND 62, SEQ ID NOs: 63 and 64, SEQ ID NOs: 65 and 66, SEQ ID NOs: 67 and 68, SEQ ID NOs: 69 and 70, SEQ ID NOs: 71 and 72, SEQ ID NOs: 73 and 74, SEQ ID NOs: 77 and 78, SEQ ID NOs: 79 and 80, SEQ ID NOs: 81 and 82, SEQ ID NOs: 83 and 84, SEQ ID NOs: 87 and 88, SEQ ID NOs: 89 and 90, SEQ ID NOs: 91 and 92, SEQ ID NOs: 93 and 94, SEQ ID NOs: 95 and 96, SEQ ID NOs: 97 and 98, SEQ ID NOs: 103 and 104, SEQ ID NOs: 105 and 106, SEQ ID NOs: 107 and 108, SEQ ID NOs: 109 and 110, SEQ ID NOs: 111 and 112, SEQ ID NOs: 113 and 114, SEQ ID NOs: 115 and 116, SEQ ID NOs: 117 and 118, SEQ ID NOs: 199 and 200, SEQ ID NOs: 201 and 202, SEQ ID NOs: 203 and 204, SEQ ID NOs: 205 and 206, SEQ ID NOs: 207 and 208, SEQ ID NOs: 209 and 210, SEQ ID NOs: 211 and 212, SEQ ID NOs: 213 and 214, SEQ ID NOs: 215 and 216, SEQ ID NOs: 217 and 218, SEQ ID NOs: 219 and 220, SEQ ID NOs: 221 and 222, SEQ ID NOs: 224 and 225, SEQ ID NOs: 227 and 228, SEQ ID NOs: 227 and 228, SEQ ID NOs: 230 and 231.

Also provided are kits that include one or more of the aforementioned pairs of primers.

BRIEF DESCRIPTION OF THE FIGURES

FIGS. **1**A-**1**DD set forth the nucleotide sequences for SEQ ID NOs: 1-54. Sequences are presented in accordance with convention from left to right and top to bottom.

FIGS. **2**A-**2**KK set forth the nucleotide sequences for SEQ ID NOs: 119-198. Sequences are presented in accordance with convention from left to right and top to bottom.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides a method of diagnosing cancer by assaying for the methylation of one or more CpG islands that are indicative of cancer. Cancer can include, for example, lung, liver, pancreas, head and neck, throat, thyroid, esophagus, brain, ovarian, kidney, skin, colorectal, and hematopoeietic (e.g., lymphomas and leukemic) cancer. Generally, the method comprises providing a biological sample from a subject in need of cancer diagnosis and assaying the sample for methylation of a CpG island associated with at least one gene selected from the group consisting of: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, HTR1A, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, FLJ36980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, ISL2, KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, MMP9, TNFSF11, RHOD or LRRC49. In preferred embodiments, the method can include assaying for methylation of CpG islands associated with two, three, four, five, six, seven, eight, nine, ten, eleven, or more of the foregoing genes. Methylation of the CpG islands associated with these genes is indicative of cancer.

The invention further provides a method of diagnosing prostate cancer by assaying for the methylation of one or more CpG islands that are indicative of prostate cancer in a male mammal. In one embodiment, the method comprises providing a biological sample from a male mammal in need of cancer diagnosis and assaying the sample for methylation of a CpG island associated with at least one gene selected from the group consisting of: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4,

HTR1A, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, FLJ36980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, HTRA4, MMP9, TNFSF11, RHOD and LRRC49. For example, the method of diagnosing prostate cancer includes assaying the biological sample for methylation of a CpG island associated with NRG1, KIF13B, or both. In another example, the method includes assaying for methylation of a CpG island associated with at least one gene selected from the group consisting of: TDH, ASAH1, FGF20, HEMK1, PALD NEUROG, EFHA2, KIFC2, GFRA1, DKK2, TNFSF11, NTN1, and RHOD. In preferred embodiments, the method of diagnosing prostate cancer can include assaying for methylation of CpG islands associated with two, three, four, five, six, seven, eight, nine, ten, eleven, or more of the foregoing genes. Methylation of the CpG islands associated with these genes is indicative of cancer.

The foregoing method of diagnosing prostate cancer can optionally include, in combination with assaying for methylation of CpG islands associated with the foregoing genes, further assaying the biological sample for methylation of a CpG island associated with at least one gene that is known to be (i) methylated in prostate cancer and (ii) not detectably methylated or methylated at a lower level (e.g., about 50% or less, about 40% or less, about 30% or less, about 20% or less, or less than about 10%) in BPH. In this regard, when the method includes assaying for at least one CpG island that is known to be methylated in prostate cancer but is known not to be detectably methylated or methylated at a lower level in BPH, the method preferably includes assaying the biological sample for methylation of CpG islands associated with at least three different genes. Examples of CpG islands known to be methylated in prostate cancer but not detectably methylated or methylated at a lower level in BPH include CpG islands associated with glutathione S-transferase P1 (GSTP1), glutathione peroxidase 3 (GPX3), glutathione S-transferase M1 (GSTM1), glutathione S-transferase M4 (GSTM4), Cub and Sushi multiple domains1 (CSMD1), tumor necrosis factor receptor superfamily member 10A (TNFRSF10A) tumor necrosis factor receptor superfamily member 10B (TNFRSF10B), tumor necrosis factor receptor superfamily member 10C (TNFRSF10C), tumor necrosis factor receptor superfamily 10D (TNFRSF10D), secreted frizzled-related protein 1 (SFRP1), secreted frizzled-related protein 2 (SFRP2), dickkopf homolog 3 (DKK3), prostaglandin-endoperoxide synthase 2 (PTGS2), cyclin-dependent kinase inhibitor 1C (CDKN1C/p57), Ras association (Ra1GDS/AF-6) domain family 1 (RASSF1), and G-protein coupled receptor 62 (GPR62).

The invention also provides a method of prognosticating cancer by assaying for the methylation of one or more genes that are indicative of the grade or stage of the cancer, and/or the length of disease-free survival following treatment for cancer. Generally, the method comprises providing a biological sample from a subject in need of cancer prognosis and assaying the sample for methylation of a CpG island associated with at least one gene selected from the group consisting of: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, HTR1A, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, F1136980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, ISL2, KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, MMP9, TNFSF11, RHOD and LRRC49. In preferred embodiments, the method can include assaying for methylation of CpG islands associated with two, three, four, five, six, seven, eight, nine, ten, eleven, or more of the foregoing genes. Methylation of the CpG islands associated with these genes is indicative of the grade or stage of the cancer, and/or the length of disease-free survival following treatment for cancer.

The invention also provides a method of prognosticating prostate cancer in a male mammal by assaying for the methylation of one or more CpG islands that are indicative of the grade or stage of the prostate cancer, and/or the length of disease-free survival following treatment for prostate cancer. In one embodiment, the method comprises assaying a biological sample from the male mammal for methylation of a CpG island associated with at least one of the following genes: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, HTRIA, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, F1136980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, or ISL2. In addition to or instead of the foregoing, the method can include assaying the biological sample for methylation of a CpG island associated with at least one of the following genes: KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, RASSF5, HTRA4, MMP9, TNFSF11, RHOD or LRRC49. For example, the method of diagnosing prostate cancer includes assaying the biological sample for methylation of a CpG island associated with NRG1, KIF13B, or both. In another example, the method includes assaying for at least one of the following genes: TDH, ASAH1, FGF20, HEMK1, PALD NEUROG, EFHA2, KIFC2, GFRA1, DKK2, TNFSF11, NTN1, or RHOD. In preferred embodiments, the method of diagnosing prostate can include assaying for methylation of CpG islands associated with two, three, four, five, six, seven, eight, nine, ten, eleven, or more of the foregoing genes. Methylation of the CpG islands associated with these genes is indicative of the grade or stage of prostate cancer, and/or the length of disease-free survival following treatment for prostate cancer.

The foregoing method of prognosticating prostate cancer can optionally include, in combination with assaying for methylation of CpG islands associated with the foregoing genes, further assaying the biological sample for methylation of a CpG island associated with at least one gene that is known to be (i) methylated in prostate cancer and (ii) not detectably methylated or methylated at a lower level (e.g., about 50% or less, about 40% or less, about 30% or less, about 20% or less, or less than about 10%) in BPH. Percent methylation level in BPH refers to the percent of patients that exhibit some detectable level of methylation at that locus. In this regard, when the method includes assaying for methylation of at least one CpG island that is known to be methylated in prostate cancer but is known not to be detectably methylated or is methylated at a lower level in BPH, the method preferably includes assaying the biological sample for methylation of CpG islands associated with at least three different genes. Examples of CpG islands known to be methylated in prostate cancer but not detectably methylated or methylated at a lower level in BPH include CpG islands associated with GSTP1, GPX3, GSTM1, GSTM4, CSMD1, TNFRSF10A, TNFRSF10B, TNFRSF10C, TNFRSF10D, SFRP1, SFRP2, DKK3, PTGS2, CDKN1C/p57, RASSF1, and GPR62. Methylation of CpG islands associated with the genes is indicative of the grade or stage of the prostate cancer, and/or the length of disease-free survival following treatment for prostate cancer.

Obtaining information about the aggressiveness of the cancer, its grade, and its stage is helpful when choosing a course of treatment. The patterns of CpG methylation may be correlated to the pathological stage and grade of the tumor. For example, in prostate cancer, patterns of CpG methylation may be correlated to the Gleason score of the primary tumor. The molecular information derived from CpG methylation may also be correlated to the likelihood of survival and the length of disease-free survival following treatment. The above prognostic methods can enable the prediction of the course of the cancer, as well as the prediction of the best approach to treatment.

Also provided are methods of assessing the efficacy of treatment of cancer by assaying for the reduced methylation of CpG islands that indicates efficacy of treatment. Generally, the method comprises providing a first and a second biological sample from a subject in need of assessing the efficacy of treatment of cancer and assaying the samples for a change in methylation level of a CpG island associated with at least one gene selected from the group consisting of: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, HTR1A, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, F1136980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, ISL2, KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, MMP9, TNFSF11, RHOD and LRRC49. Generally, the first biological sample is taken (e.g, prior to commencing treatment or during treatment) before the second biological sample, and the second biological sample is taken after a course of treatment. In preferred embodiments, the method includes assaying for a change in methylation of CpG islands associated with two, three, four, five, six, seven, eight, nine, ten, eleven, or more of the foregoing genes. A decrease or absence of methylation of the assayed one or more CpG islands in the second sample (i.e., following the course of treatment) indicates that the treatment is effective. Alternatively, the maintenance or increase of methylation in the assayed CpG islands in the second sample can indicate a reduction or absence of treatment efficacy.

The invention provides a method of assessing the efficacy of treatment of prostate cancer in a male mammal by assaying for the reduced methylation of CpG islands that indicate efficacy of treatment of prostate cancer. In one embodiment, the method comprises assaying biological samples, which are taken from the male mammal periodically during the course of treatment, for methylation of a CpG island associated with at least one gene selected from the group consisting of: NRG1, ADRB3, GFRA2, KIF13B, RET, GPR147, NEUROG3, PALD, HEMK1, FGF4, HTR1A, RNF180, DKFZP5640822, ZNF596, LOC441320, TDH, F1136980, FGF20, EFHA2, ASAH1, NODAL, LOC399783, and ISL2. In addition to or instead of the foregoing, the method can include assaying the biological samples for methylation of a CpG island associated with at least one gene selected from the group consisting of: KIFC2, C20orf23, GFRA1, GPX7, DKK2, NTN1, RASSF5, HTRA4, MMP9, TNFSF11, RHOD and LRRC49. For example, the method of assessing the efficacy of treatment of prostate cancer includes assaying the biological sample for methylation of a CpG island associated with NRG1, KIF13B, or both. In another example, the method includes assaying for a CpG island associated with at least one gene selected from the group consisting of: TDH, ASAH1, FGF20, HEMK1, PALD NEUROG, EFHA2, KIFC2, GFRA1, DKK2, TNFSF11, NTN1, and RHOD. In preferred embodiments, the method can include assaying for methylation of CpG islands associated with two, three, four, five, six, seven, eight, nine, ten, eleven, or more of the foregoing genes. Generally, the assayed biological samples in the method include a first and a second biological sample. The first biological sample can be taken, for example, prior to commencing treatment or during treatment, though in any event prior to taking the second biological sample. The second biological sample is taken during or after a course of treatment. A decrease or absence of methylation of the assayed one or more CpG islands in the second sample (i.e., following the course of treatment) as compared to the first sample indicates that the treatment is effective. Alternatively, the maintenance or increase of methylation in the assayed CpG islands in the second sample as compared to the first sample can indicate a reduction in or absence of treatment efficacy.

The foregoing method of assessing the efficacy of prostate cancer treatment can optionally include, in combination with assaying for methylation of CpG islands associated with the foregoing genes, further assaying the biological sample for reduced methylation of a CpG island associated with at least one gene that is known to be (i) methylated in prostate cancer and (ii) not detectably methylated or methylated at a lower level (e.g., about 50% or less, about 40% or less, about 30% or less, about 20% or less, or less than about 10%) in BPH. In this regard, when the method includes assaying the biological samples for methylation of at least one CpG island that is known to be methylated in prostate cancer but known not to be detectably methylated or methylated at a lower level in BPH, the method preferably includes assaying for methylation of CpG islands associated with at least three different genes. Examples of CpG islands known not to be methylated in prostate cancer but not detectably methylated or methylated at a lower level in BPH include GSTP1, GPX3, GSTM1, GSTM4, CSMD1, TNFRSF10A, TNFRSF10B, TNFRSF10C, TNFRSF10D, SFRP1, SFRP2, DKK3, PTGS2, CDKN1C/p57, RASSF1, and GPR62. A decrease or absence of methylation of the CpG islands associated with the assayed genes in the second sample as compared to the first sample following some or all of the course of treatment indicates that the treatment is effective. Alternatively, the maintenance or increase of methylation in the assayed CpG islands in the second sample as compared to the first sample can indicate a reduction or absence of treatment efficacy.

CpG islands (Bird, Nature 321: 209-213 (1986); and Gardiner-Garden et al., J. Molec. Biol. 196: 261-282 (1987)) comprise about 1% of vertebrate genomes and account for about 15% of the total number of CpG dinucleotides. CpG islands typically are between about 0.2 and about 2.0 kb in length. They can be located upstream of (e.g., in a promoter or enhancer region) of the coding sequence of the associated genes or they may also extend into or be found within gene-coding regions of their associated genes. A gene-coding region can include exons and introns. Use of the phrase “associated with” to describe a CpG island’s relation to a gene, is intended to encompass CpG islands that are upstream of gene coding sequences as well as internal CpG islands. For example, the CpG island associated with the RET gene is internal and not expected to affect the expression of the RET gene when methylated. Some CpG islands are associated with the promoter of two genes and it can affect the expression of both genes. CpGs were labeled based on their location with respect to the nearest gene. In some cases, a CpG island may be located near the promoter of two different genes and may in this case influence the expression of both genes. In such case, the CpG island was named after one of the genes. For example, the LRRC49 CpG island is also associated with the THAP domain containing 10 (THAP10) gene. A CpG island can also be associated with a pseudogene or be located in a genomic region that includes no known genes or pseudogenes. The CpG island can still be of interest so long as its methylation status correlates with a disease status.

A CpG island can be separated by up to 25 kilobases (kb) (e.g., up to 20 kb, up to 19 kb, up to 18, kb, up to 17 kb, up to 16 kb, up to 15 kb, up to 10 kb, up to 9 kb, up to 8 kb, up to 7 kb, up to 6 kb, up to 5 kb, up to 4 kb, up to 3 kb, up to 2 kb, or up to 1 kb) from the transcription start site for the nearest gene and still be considered “associated with” the gene. Preferably, CpG islands associated with at least three genes are assayed. However, CpG islands associated with 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or even more genes can be assayed.

Methods of identifying CpG islands have been described (e.g., Takai et al., *Proc. Nat'l. Assoc. Sci. USA,* 99:3740-3745 (2002)). For example, genomic sequences can be analyzed to identify segments containing CpG islands that are at least 200 bp in length, have at least a 60% GC content, and contain at least 7% CpG dinucleotides. Preferred sequences are at least 250 bp in length, are at least 60% GC rich, and contain at least 7% CpG dinucleotides. Moreover, undesirable highly repetitive sequences can be screened out using a repeat masker that filters out sequences. Desirable sequences contain less than 50% repeats (i.e., a sequence of reduced complexity or a sequence that is present at multiple genomic locations) within the length of the identified CpG island. Preferably, the CpG island is no more than 45%, 40%, 35%, 30%, 25%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, or 11% repetitive. Most desirable sequences are no more than 10% repetitive. Examples of repetitive sequences are available, for example, at the web site for National Center for Biotechnology Information (NCBI).

"Biological sample" is intended to encompass any suitable sample that enables accurate assay of CpG island methylation. Examples of suitable biological samples include, but are not limited to, whole blood, blood plasma, blood serum, urine, saliva, cells (e.g., cells obtained from blood, such as epithelial cells), and tissue. Such samples are obtained in accordance with methods known in the art. When the biological sample is whole blood, blood plasma, or urine, preferably, CpG islands associated with more than three genes are assayed.

A CpG island is "not detectably methylated" when it is not methylated or it is methylated at a level below the level of sensitivity of the assay method employed.

"Noncancerous" tissue can be benign or normal. Alternatively, but not preferably, the tissue can be diseased, as long as it is not cancerous.

Methods of assaying methylation of CpG islands are known in the art and include, for example, restriction enzyme-based technology, such as one that employs digestion with a methylation-sensitive restriction endonuclease coupled with Southern blot analysis, methylation-sensitive enzymes and polymerase chain reaction (PCR), such as methylation-sensitive arbitrarily primed PCR (AP-PCR; see, e.g., Gonzalgo et al., *Cancer Res.,* 57: 594-599 (1997)), restriction landmark genomic scanning (RLGS; see, e.g., Plass et al., *Genomic* 58: 254-262 (1999)), methylated CpG island amplification (MCA; see, e.g., Toyota et al., *Cancer Res.,* 59: 2307-2312 (1999)), differential methylation hybridization (DMH; see, e.g., Huang et al., *Human Mol. Genet.,* 8: 459-470 (1999)), and Not I-based differential methylation hybridization (see, e.g., International Patent Publication No. WO 02/086163). Other methods are described in U.S. Pat. App. Pub. No. 2003/0170684 and International Patent Publication No. WO 04/05122.

Alternatively, cytosine conversion-based technology can be used. Such technology relies on methylation status-dependent chemical modification of CpG islands (i.e., deamination of unmethylated cytosines in CpG islands) within isolated genomic DNA or fragments thereof followed by DNA sequence analysis. Such methods employ reagents like hydrazine and bisulfite. Bisulfite treatment followed by alkaline hydrolysis is described by Olek et al., *Nucl. Acids Res.,* 24: 5064-5066 (1996); and Frommer et al., *PNAS USA,* 89: 1827-1831 (1992). The use of methylation-sensitive primers to assay methylation of CpG islands in isolated genomic DNA is described by Herman et al., *PNAS USA,* 93: 9821-9826 (1996), and in U.S. Pat. Nos. 5,786,146 and 6,265,171. Bisulfite-treated DNA can be subsequently analyzed by conventional molecular techniques, such as PCR amplification, fluorescence-based, real-time PCR (see, e.g., Eads et al., *Cancer Res.,* 59: 2302-2306 (1999); Heid et al., *Genome Res.,* 6: 986-994 (1996); and U.S. Pat. No. 6,331,393), sequencing, oligonucleotide hybridization detection, and methylation-sensitive single nucleotide primer extension (Ms-SNuPE; see, e.g., Gonzalgo et al., *Nucl. Acids Res.,* 25: 2529-2531 (1997); and U.S. Pat. No. 6,251,594).

A preferred method of assaying for methylation of a CpG island includes isolating genomic DNA (and/or fragments thereof) from a biological sample, treating the DNA under deaminating conditions that convert unmethylated cytosines to uracil, using the treated DNA as a template in a PCR reaction to amplify a target sequence that includes the CpG-island of interest, thereby producing an amplified sequence. Unmethylated cytosines in the target sequence, which are converted to uracils by the deaminating treatment, are amplified as thymines in the corresponding position of the amplified sequence. Since the sequence of the forward and the reverse strand of the CpG island lose their complimentarity after the deamination reaction, the methylation status of the CpG island can be determined by assaying one or both of the original strands by utilizing primers capable of annealing to the strand of interest.

The deamination reaction may not proceed to completion, which results in false positives. For example, deamination of DNA sequences using bisulfite salt is sensitive to the purity of the DNA, length of incubation, and the secondary structure of the denatured templates. Quantitative PCR methods can be used to assay for the efficiency of deamination. However, quantitative PCR methods are limited to assaying the conversion status within the sites where the primers and probes anneal to the template.

Quantitative PCR methods are also limited to assaying for the methylation of cytosines within the sites where the primers and probes anneal to the template. The primers and the probe only anneal efficiently to the templates that are fully converted and contain methylation at the appropriate cytosine nucleotides. Thus, they fail to provide methylation information for CpG dinucleotides that are not assayed for. The CpG islands may also be analyzed using direct sequencing following the deamination treatment. However, due to the heterogeneity of the methylation pattern within a CpG island and the presence of homopolymeric stretches within the sequence, direct sequencing of CpG islands can yield a sequencing pattern that is too noisy and complex for the available sequencing software.

To overcome these disadvantages and to minimize the overall cost of analysis for a clinical test, we developed a method to analyze the amplified sequences by termination-coupled linear amplification. The DNA is linearly amplified using a forward or a reverse primer in the presence of dNTPs and one or two dideoxynucleotides such as dideoxycytidine or dideoxyguanine. The amplified sequence can, optionally, be analyzed using only thymine and/or cytosine terminators when assaying for a methylated CpG dinucleotide (or adenine and/or guanine terminators when analyzing the amplified strand opposite to the CpG dinucleotide of interest) to make extension reaction products that terminate at thymines and/or cytosines nucleotides (or at guanine and/or adenine when assaying the opposite strand). The amplification reaction results in the generation of fragments with multiple lengths, each length of which corresponds to the distance in bases between the primer used for amplification and the position within the target sequence of a nucleotide that is complementary to the dideoxynucleotide added to the amplification reaction. Such amplification can result in the generation of 10 to 20 fragments from an average CpG island-containing amplicon of 100 to 150 bp. The extension products can be separated by size on an acrylamide gel and compared to (a) a size standard and/or (b) by comparing the fragments to those generated when fully unmethylated (PCR generated template or clones in *E. coli*) or fully methylated (enzymatically methylated in vitro) template to thereby determine the presence of cytosine (or guanine on the opposite strand) or the presence of thymine (or adenine on the opposite strand) in the amplified CpG island-containing sequence. When bisulfite is used as the deaminating agent, the amplified sequence may contain large stretches of thymine or adenine which may result in additional fragments due to the DNA polymerase slippage during amplification. Such "stutter" patterns may be minimized by selectively analyzing segments of the CpG islands that have shorter homopolymeric sequences. Stutter fragments can also be identified by analyzing the control templates.

When a fluoresent label is used to tag the primers or the dideoxynucleotides used in the terminator-coupled linear amplification, the resulting fragments may be analyzed using automated sequencing machines and software designed for determining the size of DNA fragments. In this regard, commercially available software such as GENESCAN (Applied Biosystems, Foster City, Calif.) and GENEMAPPER (Applied Biosystems) are trained to recognize and account for stutter patterns due to DNA polymerase slippage during the amplification of microsatellite repeats. Such software may also be used to account for the stutter pattern that is observed when amplifying homopolymeric stretches of DNA, as might be seen after bisulfite conversion of CpG islands. There are a number of fluorescent dyes available for the automated analysis of DNA such as but not limited to 6-carboxyfluorescein (6-FAM), Hexachlorofluorescein (HEX), VIC dye, 5-carboxytetramethylrhodamine (TAMRA), 5-carboxy-X-rhodamine, succinimidyl ester (5-ROX), 6-carboxy-2',4,7,7'-tetrachlorofluorescein (TET). The methods and equipment to determine amplicon size have been available for over a decade and in use for genetic linkage mapping, DNA identity, and forensic. For example, Applied Biosystems has a set of 5 dyes that can be used to multiplex fragments from 4 separate amplification reaction and one standard for use in linkage mapping on the ABI sequencers. Four different CpG islands from a single individual can be linearly amplified using fluorescently tagged primers, and the products pooled before analysis. Alternatively, different CpG islands from different individuals can be linearly amplified using fluorescently tagged primers, and the products pooled before analysis.

Since methylation of a particular CpG dinucleotide is not always complete in a sample, i.e., the CpG sequence is heterogenous, the methods provided herein can be advantageously used to analyze the extent of or percent methylation of a particular CpG dinucleotide site within a sample. In a preferred method, two different fluorescent-dye terminators are used for thymine and cytosine, respectively (or adenine and guanine, respectively, when analyzing the opposite strand) in a fluorescent dideoxy sequencing reaction. The relative abundance of the two dyes in same-size extension products are indicative of the relative abundance of the two nucleotides at a particular sequence position, and can thereby indicate the percent methylation of a particular CpG dinucleotide site within a CpG island. To determine the expected relative abundance of the two dyes, control reactions with a range of known ratios of fully methylated to fully unmethylated templates can be used. The data obtained from the control reactions can be used as a reference to estimate relative abundance of methylated and unmethylated cytosines in a sample.

The levels of methylation or patterns of methylation at given CpG islands can be assayed as appropriate. The assay can employ the use of a reference standard when appropriate to enable the determination of abnormal methylation. A reference standard can be determined based on reference samples obtained from age-matched noncancerous classes of adjacent tissues, and with normal peripheral blood lymphocytes. When, for example, efficacy of treatment is being assessed, the assay results of biological samples taken over the course of treatment can be compared without the use of a reference standard.

When the DNA obtained from a biological sample is in limited quantities and is not sufficient for the analysis of multiple markers, the methods described herein can include amplifying the DNA from the sample. Amplification can be done using PCR amplification or isothermal amplification methods, for example, those described in U.S. Pat. Nos. 5,854,033; 6,124,120; 6,143,495; 6,210,884; 6,642,034; 6,280,949; 6,632,609; and 6,642,034; and U.S. Pat. App. Pub. Nos. 2003/0032024; 2003/0143536; 2003/0235849; 2004/0063144; and 2004/0265897, which are incorporated herein by reference in their entirety. Isothermal amplification can include rolling circle or strand displacement amplification. Methods that combine PCR and isothermal amplification have also been described (U.S. Pat. Nos. 6,777,187; and 6,828,098; and U.S. Pat. App. Pub. Nos. 2004/0209298; 2005/0032104; and 2006/0068394, each of which is incorporated herein by reference in its entirety). U.S. Pat. App. Pub. No. 2005/0202490, which is incorporated herein by reference in its entirety, describes the use of such methods in combination with methylation-sensitive restriction enzymes to study the methylation pattern of DNA. DNA amplification can also include methylation-coupled whole genomic amplification to generate the DNA needed, such as described in U.S. Pat. App. Pub. No. 2006/0257905, which is incorporated by reference herein in its entirety. The methylation-coupled whole genomic amplification can be especially advantageous when DNA is recovered from minute biological samples or from bodily fluids such as urine or plasma.

Skilled artisans will appreciate that the various amplification methods described herein, e.g., the PCR amplification, isothermal amplification, and termination-coupled linear amplification method, can employ nucleotides, nucleotide analogues, nucleotide or nucleotide analogue derivatives, and/or combinations thereof.

If desired, mRNA and protein levels can be assayed, and alterations in their expression levels can be indicative of a change in the level of methylation or the patterns of methylation at given CpG islands. Such methods of assaying mRNA and protein levels are also within the skill in the art. For example, the mRNA assay methods described in U.S. Provisional Patent Application No. 60/705,964 filed on Aug. 5, 2005 and International Patent Publication No. WO 2007/019444, which are hereby incorporated by reference, can be used. Such methods are particularly useful if a degraded tissue sample is used as the biological sample. Alternatively, reverse transcription with gene-specific primers can be used to assay mRNA levels. Proteins levels can be assayed, for example, using antibody and staining techniques.

It is important to note that even though aberrant methylation of a CpG island can affect expression of the associated gene, the methods described herein are not dependent on a biological role for the hypermethylation. That is a hypermethylated CpG island can be useful in the methods of the invention regardless of its effect on gene expression. Accordingly, the only requirement is that there be a correlation between the methylated state of a CpG island and the presence of cancer.

The invention further provides target sequences and corresponding primers or probes that are useful in the above methods. The target sequences provide the context for the selection of CpG islands to assay for methylation. If a given target sequence contains more than one CpG island, all or less than all of the CpG islands, even one CpG dinucleotide, can be assayed for methylation with respect to that particular target sequence. In this regard, a target sequence can include a genomic sequence that is fully methylated and fully deaminated such as SEQ ID NO: 1 or 2 [NRG1], SEQ ID NO: 3 or 4 [ADRB3], SEQ ID NO: 5 or 6 [GFRA2], SEQ ID NO: 7 or 8 [KIF13B], SEQ ID NO: 9 or 10 [RET], SEQ ID NO: 11 or 12 [GPR147], SEQ ID NO: 13 or 14 [NEUROG3], SEQ ID NO: 15 or 16 [PALD], SEQ ID NO: 17 or 18 [HEMK1], SEQ ID NO: 19 or 20 [FGF4], SEQ ID NO: 23 or 24 [HTR1A], SEQ ID NO: 25 or 26 [RNF180], SEQ ID NO: 27 or 28 [ECOP], SEQ ID NO: 29 or 30 [ZNF596], ID NO: 33 or 34 [LOC441320], SEQ ID NO: 35 or 36 [TDH], SEQ ID NO: 37 or 38 [FLJ36980], SEQ ID NO: 39 or 40 [FGF20], SEQ ID NO: 41 or 42 [EFHA2], SEQ ID NO: 43 or 44 [ASAH1], SEQ ID NO: 45 or 46 SEQ ID NO: 49 or 50 [NODAL], SEQ ID NO: 51 or 52 [LOC399783], SEQ ID NO: 53 or 54 [ISL2]. These fully methylated and deaminated sequences are used for illustrative purposed and do not exclude the use of partially methylated and deaminated sequences in the methods of the invention. A target sequence can include a genomic sequence that is partially methylated, such as in DNA obtained from a tumor, and then deaminated such that the target differs from the sequence listed above. Persons of skill in the art will appreciate that a target sequence that includes a partially methylated and deaminated CpG island will result in a population of DNA molecules that differ at one or more positions that correspond to the cytosine residues in one or more CpG dinucleotides. Thus, a target sequence can include a variety of partially methylated and deaminated sequences based on the following genomic sequences SEQ ID NOs: 119 or 220 [KIFC2], SEQ ID NOs: 121 or 122 [C200RF23], SEQ ID NOs: 123 or 124 [GFRA1], SEQ ID NOs: 129 or 130 [DKK2], SEQ ID NOs: 133 or 134 [RASSF5], SEQ ID NOs: 135 or 136 [NTN1], SEQ ID NOs: 139 or 140 [GPR147], SEQ ID NOs: 141 or 142 [NEUROG3], SEQ ID NOs: 143 or 144 [NODAL], SEQ ID NOs: 145 or 146 [PALD], SEQ ID NOs: 147 or 148 [LOC399783], SEQ ID NOs: 151 or 152 [LOC441320], SEQ ID NOs: 153 or 154 [ZNF596], SEQ ID NOs: 155 or 156 [TDH], SEQ ID NOs: 157 or 158 [ASAH1], SEQ ID NOs: 159 or 160 [FGF20], SEQ ID NOs: 161 or 162 [FLJ36980], SEQ ID NOs: 163 or 164 [GFRA2], SEQ ID NOs: 165 or 166 [EFHA2], SEQ ID NOs: 171 or 172 [KIF13B], SEQ ID NOs: 173 or 174 [ADRB3], SEQ ID NOs: 175 or 176 [NRG1], SEQ ID NOs: 177 or 178 [ECOP], SEQ ID NOs: 179 or 180 [HTR1A], SEQ ID NOs: 181 or 182 [ISL2], SEQ ID NOs: 183 or 184 [LOC285671], SEQ ID NOs: 185 or 186 [FGF4], SEQ ID NOs: 189 or 190, [HEMK1], SEQ ID NOs: 191 or 192 [RET] SEQ ID NOs: 193 or 194 [HTRA4], SEQ ID NO: 195 [RHOD], SEQ ID NO: 196[TNFSF11], SEQ ID NO: 197 [MMP9], and SEQ ID NO: 198 [LRRC49].

These targets can be used in combination with known targets (for example known CpG islands associated with GSTP1, GPX3, GSTM1, GSTM4, CSMD1, TNFRSF10A, TNFRSF10B, TNFRSF10C, TNFRSF10D, SFRP1, SFRP2, DKK3, PTGS2, CDKN1C/p57, RASSF1, and GPR62. For example, fully methylated and deaminated sequences for some of these genes are provided in SEQ ID NO: 31 or 32 [CSMD1], SEQ ID NO: 45 or 46 [TNFRSF10C], SEQ ID NO: 47 or 48 [TNFRSF10B] SEQ ID NO: 21 and 22 [GPR62]. Also for example, a target sequence can include fully or partially methylated and (subsequently) deaminated sequences based on the following genomic sequences SEQ ID NOs: 131 or 132 [GPX3], SEQ ID NOs: 125 or 126 [GPX7], SEQ ID NOs: 127 or 128 [GSTM4], SEQ ID NOs: 137 or 138 [SFRP2], SEQ ID NOs: 149 or 150 [CSMD1], SEQ ID NOs: 167 or 168 [TNFRSF10B], SEQ ID NOs: 169 or 170 [TNFRSF10C], and SEQ ID NOs: 187 or 188 [GPR62]. Such target sequences can be isolated or purified in accordance with methods known in the art.

Also provided are isolated or purified primers derived from and suitable for amplifying sequences internal to the above isolated or purified nucleic acid molecules. The isolated or purified primers can be DNA, RNA, PNA, and the like. It will be understood by one of ordinary skill in the art, however, that one type of nucleic acid can be preferred over another, depending on the particular biological sample, the methodology employed in assaying CpG islands for methylation, and the ability of the particular type of nucleic acid to detect methylation. One or more (e.g., two, three four, four, five, six, seven, eight, nine ten or more) isolated pairs of primers can be provided. Optionally, primers are provided as part of a kit useful in the methods disclosed herein. The pair of primers can consist essentially of SEQ ID NOs: 55 and 56, SEQ ID NOs: 57 and 58, SEQ ID NOs: 59 and 60, SEQ ID NOs: 61 AND 62, SEQ ID NOs: 63 and 64, SEQ ID NOs: 65 and 66, SEQ ID NOs: 67 and 68, SEQ ID NOs: 69 and 70, SEQ ID NOs: 71 and 72, SEQ ID NOs: 73 and 74, SEQ ID NOs: 75 and 76, SEQ ID NOs: 77 and 78, SEQ ID NOs: 79 and 80, SEQ ID NOs: 81 and 82, SEQ ID NOs: 83 and 84, SEQ ID NOs: 85 and 86, SEQ ID NOs: 87 and 88, SEQ ID NOs: 89 and 90, SEQ ID NOs: 91 and 92, SEQ ID NOs: 93 and 94, SEQ ID NOs: 95 and 96, SEQ ID NOs: 97 and 98, SEQ ID NOs: 99 and 100, SEQ ID NOs: 101 and 102, SEQ ID NOs: 103 and 104, SEQ ID NOs: 105 and 106, or SEQ ID NOs: 107 and 108. It is understood that these primer pairs are examples of suitable primers for use in the context of the invention. For example, each primer can be between 10 and 40 nucleotides and together the pair of primers can flank a region of at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120, 130, 140, 150, 200, 250, 300 by in length that includes one or more CpG dinucloetides in a CpG island of interest. Primer pairs can be modified in various ways, such as by chemical modification of a base, and still be useful in the context of the invention. Other primers derived from the target sequences, namely SEQ ID NOs: 1-54 and 119-198, and variants thereof, also can be used in the context of the invention. The only requirement is that such primers function to assay for methylation of a given CpG island. Thus, for example, alternate primers can be selected or the provided primers can be modified or provided in degenerate form to account for target sequence polymorphisms within a given population, so long as the primers are still suitable for assaying modification of CpG islands associated with the genes disclosed herein.

Like the target sequences, the primer pairs can be isolated or purified in accordance with methods known in the art. Alternatively, they can be synthesized using routine methods.

The primers can be part of a kit. Preferably, the kit comprises at least three pairs of primers, wherein each primer pair is specific for a CpG island associated with a different gene. However, the kit can comprise additional primer pairs, such as primer pairs for other CpG islands associated with the same gene or primer pairs for amplifying CpG islands associated with four, five, six, seven, eight, nine, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27 or even more genes. The kit can further comprise one or more reagents for assaying for methylation of CpG islands, instructions for use, and/or other components as are typically found in kits. For example, the kit can comprise a buffer suitable for (a) isolating genomic DNA comprising a target sequence from a biological sample, (b) amplifying a portion of the target sequence, and/or (c) deaminating a target sequence. In embodiments directed to the evaluation of prostate cancer, a kit can comprise one or more buffers suitable for preparing genomic DNA from serum and/or urine samples.

EXAMPLES

The following examples serve to illustrate the invention. The examples are not intended to limit the scope of the invention.

Example 1

This example demonstrates the determination of the methylation status of markers based on methylation-specific PCR amplification. Paraffin-embedded prostate tissues were obtained following radical prostatectomies. The tissue samples were sectioned into 23 10-micron sections and slide 1, 12, and 23 were stained using hematoxylin and eosin (H&E). Using the H&E slides as guide, the areas corresponding to the tumor tissues were microdissected from the unstained slides. The remaining tissues were recovered to use as a normal paired sample. Following deparaffinization using two xylene extractions and two ethanol washes, the DNA was isolated from the tumor tissue and surrounding normal tissues using standard proteinase K digest for 5 days at 50° C., extraction with phenol/chloroform and ethanol precipitation (*Current Protocols in Molecular Biology*, edited by Ausubel, et al., Wiley-Interscience (New York 1988, revised 1988-2006)). The DNA was resuspended in TE8 and the quality and quantity of the DNA was assessed by agarose gel electrophoresis using concentration and size standards as reference. Following denaturation in the presence of 0.3 M NaOH, the DNA was treated with 2.5 M sodium metabisulfite, pH 5.5, in the presence of 1 mM hydroquinone at a concentration of 1 μg of DNA/500 μl. The reaction was incubated in a thermocycler for a total of 8 cycles (95° C. for 5 minutes; 55° C. for 115 minutes).

Following bisulfite treatment, the DNA was purified using the QIAEX II purification kit (Qiagen, Valencia, Calif.) according to the manufacturer's recommendations and eluted in 50 μl of TE8. Sodium hydroxide (5.5 μl of 2 N) was added, and the DNA was incubated at RT for 15 min. The DNA was then precipitated with 3 volumes of ethanol and 0.3 volumes of 5 M NH_4OAC. The DNA was resuspended in 50 μl of TE8 and stored at −20° C.

In order to determine if a specific CpG position is methylated in genomic DNA isolated from tumor tissue, methylation-specific polymerase chain reaction (PCR) was performed, using primers designed to overlap the position of the CpG island of interest. All PCR reactions were performed in a MASTERCYCLER thermocycler (Eppendorf, Westbury, N.Y.) for 42 cycles of 95° C. for 15 seconds, 63° C. for 30 seconds, and 72° C. for 10 seconds. Each reaction was carried out in 30 μl of 1× PLATINUM Taq PCR buffer containing 1.5 mM magnesium chloride, 0.25 mM dNTPS, 12.5 pmoles of each primer, and 0.5 units of PLATINUM Taq enzyme (Invitrogen, Carlsbad Calif.). The primers used for each CpG island and the size of the product are shown in Table 1, wherein "F" indicates forward primer, "R" indicates reverse primer, "m" indicates methylated, and "u" indicates unmethylated.

TABLE 1

Gene associated with CpG island	Primer sequences	Annealing temperature (° C.)	Product size (bp)
NRG1	mF: GAGCGGGTAGCGAGAGTTTCGG [SEQ ID NO: 55] mR: TAACGACGCGACTACCGAAAACC [SEQ ID NO: 56]	63	119
ADRB3	mF: GATTAACGTGTTCGTGATTTCGTT [SEQ ID NO: 57] mR: CAACGACCAATAACCAATCAACGCC [SEQ ID NO: 58]	63	102
GFRA2	mF: ATACGTCGGTGAGTTCGGTTTATC [SEQ ID NO: 59] mR: ACTCCCGACTCCCTAAACTCCGAA [SEQ ID NO: 60]	63	101
KIF13b	mF: TGAATCGGCGAGGTGAGAGTCG [SEQ ID NO: 61] mR: ACCGAACGTCTCAACGCGAAAACG [SEQ ID NO: 62]	65	179
RET	mF: TATCGTTAGCGTCGTGGTGGAGTT [SEQ ID NO: 63] mR: CTACACGAACACTAAACCGACCGA [SEQ ID NO: 64]	63	120
GPR147	mF: TCGGTCGTTACGTTGATCGTTATTC [SEQ ID NO: 65] mR: ACCCTACGCATACCCTTCTCGAAC [SEQ ID NO: 66]	63	119
NEUROG3	mF: GTTTCGAGGAAGTTTCGGGTACGG [SEQ ID NO: 67]	63	103

TABLE 1-continued

Gene associated with CpG island	Primer sequences	Annealing temperature (° C.)	Product size (bp)
	mR: GATCGTTAACCTTCTTTCGCCGAC [SEQ ID NO: 68]		
PALD	mF: CGAAGTTGGGAGGAGCGAGTT [SEQ ID NO: 69] mR: AAACATCCGTACTCCTACGACCGA [SEQ ID NO: 70]	63	115
HEMK	[tiF: CGTATTAGTCGTATTCGCGAGCGT [SEQ ID NO: 71] mR: CGAAACTACTCGACCCGACCC [SEQ ID NO: 72]	63	99
FGF4	mF: TAACGGTACGTTGGAGGTCGAGTT [SEQ ID NO: 73] mR: ACGACCGCCTCCTTAAACTACGCT [SEQ ID NO: 74]	63	102
GPR62	mF: TATCGTGTATTCGTTGCGGTTAGG [SEQ ID NO: 75] mR: AACGATACGAACGACGTACCGAA [SEQ ID NO: 76]	63	120
HTR1A	mF: TACGTGAATAAGAGGACGTTTCGG [SEQ ID NO: 77] mR: AACGATCTTCCGAAATACGCCAA [SEQ ID NO: 78]	63	115
RNF180	mF: TCGTCGAATCGGTATCGTCGTC [SEQ ID NO: 79] mR: ACCTATATCCACGTCCCGAAACCT [SEQ ID NO: 80]	63	118
ECOP	mF: CGGTTGTAGTTTGTTCGTTCGTTTC [SEQ ID NO: 81] mR: CTAACGCCTCATAACTCCTCGCGT [SEQ ID NO: 82]	63	108
ZNF596	mF: GCGTCGATTCGGGAGTAGTATCGT [SEQ ID NO: 83] mR: ATACCGTAAATCCGCGCTACTTCC [SEQ ID NO: 84]	63	96
CSMD1	mF: CGTTGAGGTCGAATGAAGCGTAGT [SEQ ID NO: 85] mR: AACCGAAACTAAACACGACGCAA [SEQ ID NO: 86]	63	96
LOC441320	mF: AAGCGTATAGTTCGAGGATTGCGA [SEQ ID NO: 87] mR: CCGCGTCACTTACTCCTCTACGA [SEQ ID NO: 88]	63	107
TDH	mF: CGTTGGGTGCGTAGGAAGGTTAGT [SEQ ID NO: 89] mR: GACCGACCCTAAACAACCCGCT [SEQ ID NO: 90]	63	120
FLJ36980	mF: GTTGCGGGATAGCGTTGTGATT [SEQ ID NO: 91] mR: ACCATTATCAATACTCCGATCGCC [SEQ ID NO: 92]	63	96
FGF20	mF: TTTGTTTGTTAAGGGCGTTATCGT [SEQ ID NO: 93] mR: CCGCGACTACTCTAACCAACCC [SEQ ID NO: 94]	63	105
EFHA2	mF: GGGCGTTGAGTTTAGTTCGGAGA [SEQ ID NO: 95] mR: ACGAACACAACCGAATCAACGTAA [SEQ ID NO: 96]	63	108

TABLE 1-continued

Gene associated with CpG island	Primer sequences	Annealing temperature (° C.)	Product size (bp)
ASHA1	mF: GGCGTTGGTTGTTAGAGCGATG [SEQ ID NO: 97] mR: GACTCAAACTCACTCACCGACGAC [SEQ ID NO: 98]	63	114
TNFRSF10C	mF: GGTGCGATTTAGGATTTAGGACGG [SEQ ID NO: 99] mR: GCGACCGAAACTCACTAACAACAA [SEQ ID NO: 100]	63	115
TNFRSF10B	mF: GCGATTTGGGTCGTTAGGGAATAG [SEQ ID NO: 101] mR: ACCTCTCCGTAACTTCACGCAACTT [SEQ ID NO: 102]	63	119
NODAL	mF: GGTAGTCGCGGTCGTTTACGTT [SEQ ID NO: 103] mR: ACGAACAAACGACAAATCGAATCA [SEQ ID NO: 104]	63	111
LOC399783	mF: TACGTTGAGTTCGGTTTGGTTTGT [SEQ ID NO: 105] mR: CGCGCCTCCGTAATCTAAACTAA [SEQ ID NO: 106]	63	103
ISL2	mF: GTGCGTGTTGACGTTATGTTGCGT [SEQ ID NO: 107] mR: CGCCCGACCTCGACTCTTTACT [SEQ ID NO: 108]	63	99
GSTP1	mF: CGGCGATTTCGGGGATTTTAGGGC [SEQ ID NO: 109] mR: GACCGCTCTTCTAAAAAATCCCGCG [SEQ ID NO: 110]	63	109
GSTP1	mF: ACGTTCGGGGTGTAGCGGTCGTC [SEQ ID NO: 111] mR: CCCCAATACTAAATCACGACGCCG [SEQ ID NO: 112]	63	93
GSTP1	mF: GGTCGGCGTCGTGATTTAGTATTGG [SEQ ID NO: 113] mR: ACTACGACGACGAAACTCCAACGA [SEQ ID NO: 114]	63	99
GSTP1	uF: TGTGGTGATTTTGGGGATTTTAGGGT [SEQ ID NO: 115] uR: CCAACCACTCTTCTAAAAAATCCCACA [SEQ ID NO: 116]	63	113
GSTP1	uF: GATGTTTGGGGTGTAGTGGTTGTTG [SEQ ID NO: 117] uR: CTCCACCCCAATACTAAATCACAACA [SEQ ID NO: 118]	63	99
KIFC2	mF: TGATGGTCGTATTGCGGGTTTATC [SEQ ID NO: 199] mR: ATACCTAAACCCAACGCCGACTAC [SEQ ID NO: 200]	62	91
C20orf23	mF: CGCGATTTGAGTAGTTAGCGTCGT [SEQ ID NO: 201] mR: AACCAACGCGACGACCTAACTAAC [SEQ ID NO: 202]	62	90
GFRA1	mF: TAGATTTCGGTGTTTCGGGCGTT [SEQ ID NO: 203] mR: CCGCTAATTCCCAATCGTACTACTCA [SEQ ID NO: 204]	62	98
GPX7	mF: TTCGTTTCGTTCGGTCGTGATT [SEQ ID NO: 205] mR: GACTACGAACGCTTCGAATTCCTC [SEQ ID NO: 206]	62	116

TABLE 1-continued

Gene associated with CpG island	Primer sequences	Annealing temperature (° C.)	Product size (bp)
DKK2	mF: GTTGCGTTGGTAGCGATTCGTTGT [SEQ ID NO: 207] mR: CCCGAACCGAATCCTCGAAATCT [SEQ ID NO: 208]	62	117
NTN1	mF: GACGTAGTATGATGCGCGTAGTGTG [SEQ ID NO: 209] mR: GCGAACATACTAAACCCGAACCC [SEQ ID NO: 210]	62	103
HTRA4	mF: GGATTACGTCGGTGTTCGATTTGT [SEQ ID NO: 211] mR: AACGCACGATTAACCCTACGCC [SEQ ID NO: 212]	62	95
MMP9	mF: TCGGATTAAGGTAGGCGTGGTTTC [SEQ ID NO: 213] mR: AACGTAAACGCCGAACCGAAC [SEQ ID NO: 214]	62	102
RHOD	mF: GGAAGACGTCGTTGTTGATGGTTT [SEQ ID NO: 215] mR: ACCGCTCCGACACGAACCTATAC [SEQ ID NO: 216]	62	120
TNSF11	mF: AGCGTTATGCGTCGCGTTAGTAG [SEQ ID NO: 217] mR: GCAAACGACGACGAAACGTACA [SEQ ID NO: 218]	62	116
SFRP2	mF: GAAGAGAGCGGGTTCGGGATAAG [SEQ ID NO: 219] mR: CTACAACATCGTAAACGCGCGAC [SEQ ID NO: 220]	62	101

The products of the PCR reactions were separated on 8% acrylamide gel. Only templates that exhibited methylation at all of the CpG islands that were present within the primers could serve as efficient templates for the amplification reactions. Control reactions were performed using fully methylated templates that were methylated in vitro using SS1 (CpG) methylase (NEB, Beverly, Mass.) according to the manufacturer's protocol. All primer pairs listed in Table 1 yielded a product of the correct size from fully methylated control template. Two negative controls (water and DNA isolated from white blood cells) were included for each target PCR amplification, which did not yield a PCR product. When a CpG island is methylated in a DNA sample, an amplification product of the expected size is obtained. This example demonstrates that the above primers can be used to assay for methylation of CpG islands in prostate cancer and that the CpG islands exhibit methylation in prostate cancer.

Example 2

This example demonstrates the determination of the methylation status of CpG islands at the ADRB3 locus by DNA sequencing. DNA is obtained from tumor samples and treated with sodium bisulfite as described in example 1. Two microliters of the bisulfite treated DNA are amplified with the following primers: ADRB3-F1: GAGAAGAGGAAGGTAGAAGGAG [SEQ ID NO: 221] and ADRB3-R1: CTACCTAACTATAACCAACCC [SEQ ID NO: 222] for 40 cycles as described in example 1 except for the annealing temperature, which is lowered to 55° C. The amplified 250 bp product is purified using QIAquick PCR purification kit (Qiagen, Valencia Calif.) and recovered in TE8. Fifty nanograms of the ADRB3 amplified product is sequenced using 1.25 pmole of ADRB3-F2:ACGGAGGAGGATAGTAGTACG [SEQ ID NO: 223] using BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems) and the sequencing reaction is purified using Centri-Sep columns (Applied Biosystems) according to the manufacturer's protocols. The products of the sequencing reaction are analyzed using an ABI 3700 sequencer according to manufacturer's specification. The resulting DNA sequence shows one or more sequence peaks corresponding to cytosine base or a mixed cytosine/thymidine base at the cytosine residue position of CpG dinucleotides that are fully or partially methylated in the original tumor DNA.

Alternatively, a more detailed sequence analysis is obtained by cloning the product of the amplification reaction using a TOPO TA cloning kit (Invitrogen, Carlsbad Calif.) according to supplier's protocol. Approximately 20 colonies are chosen for further analysis. Each colony is grown in 3 ml of LB media for 16 hours. DNA is isolated from 1.5 ml aliquot using plasmid preparation kit from Qiagen. The plasmid DNA is quantitated using spectrophotometer and 1 microgram aliquot is sequenced as described above. The sequence of the 20 individual clones is compared to determine which cytosines are methylated and to provide an estimate of their rate of methylation in the tumor sample. This example shows that the methylation status of cytosines within CpG islands can be determined using a sequencing approach.

Example 3

This example demonstrates the determination of the methylation pattern of multiple CpG islands associated with KIFC2, GFRA1 and GPX7 using terminator-coupled linear amplification. From DNA from tumor samples prepared as described in example 1, fragments of the CpG islands associated with KIFC2, GFRA1, GPX7 are amplified individually using the mF1 and mR1 primers shown below for each CpG island. The amplification reactions are performed for 42 cycles as described in example 1 except for the annealing temperature, which was lowered to 58° C. An aliquot of the amplification reaction is separated on an 8% acrylamide gel to verify that fragments of the appropriate length are obtained (264 bp for KIFC2, 326 bp for GFRA1, 367 bp for GPX7). The product of the PCR reaction were purified using QIAQUICK PCR purification kit (Qiagen).

Each amplification product (25 nanograms) is subjected to linear terminator-coupled amplification using 1.5 pmoles of the fluorescently labeled F2 primer shown below for the corresponding amplicon. The amplification reaction includes 1× VentR (exo-) DNA polymerase (New England Biolabs, Beverly Mass.), 30 μM dATP, 37 μM dCTP, 100 μM dGTP, 100 μM dTTP, 480 μM ddCTP and 2 units of VentR (exo-) DNA polymerase. Reactions are performed in an MASTERCYCLER thermocycler (Eppendorf) for 30 cycles of 95° C. for 15 seconds, 58° C. for 30 seconds, and 72° C. for 30 seconds. Following amplification, the reaction products are pooled into a single tube and purified using Centri-Sep columns (Applied Biosystems) according to the manufacturer's protocols. One microliter of GENESCAN 500 LIZ standard (Applied Biosystems) is added to one tenth of the purified fragment and the DNA separated using the ABI Prism 3100 Genetic Analyzer (Applied Biosystems) according to manufacture's instructions. The data is analyzed using the GENESCAN and the GENEMAPPER software (Applied Biosystems).

The following primers are used for the amplifications:

KIFC2-F1:
AGGTA(C/T)GTTGTATTTGGTGGATTTGG [SEQ ID NO: 224]

KIFC2-R1:
CCCACCTACAACAACAACACC [SEQ ID NO: 225]

KIFC2-F2:
6FAM-GAACGCGTACGGAAGGTAGG [SEQ ID NO: 226]

GFRA1-F1:
GTGATAGGTTTGTAGATTTGATAGTTG [SEQ ID NO: 227]

GFRA1-R1:
AACTAACCTCCATTTTAACTATTTC [SEQ ID NO: 228]

GFRA1-F2:
NED-GAGAGATGAATTTGGATATTAGT [SEQ ID NO: 229]

GPX7-F1:
GGTAAATTGGTGT(C/T)GTTGGAGAAG [SEQ ID NO: 230]

GPX7-R1:
ACTAAACAATAATACCC(A/G)ACCTC [SEQ ID NO: 231]

GPX7-F2:
VIC-GTCGTTGGGTTCGGTTTCGTTTTG [SEQ ID NO: 232]

The F1 and R1 primers are used for the amplification of a fragment of a CpG island from the tumor DNA. The F2 primers are used for termination-coupled linear amplification.

This example shows that termination-coupled linear amplification fragment lengths can be analyzed to (i) determine the presence and/or the positions of methylated cytosines in CpG islands in a sequence of interest as well as (ii) provide information about the efficiency of the deamination reaction, since incomplete deamination results in fragments with length that differ than what is expected from the positions of the CpG dinucleotides within the sequence.

Example 4

This example demonstrates the use of methylation-coupled whole genome amplification on DNA recovered from urine samples to increase the amount of DNA available for CpG island marker assays. Urine samples were obtained from 4 patients that were recently diagnosed with prostate cancer. 50 ml samples were spun down at 4000 rpm for 15 min, transferred to 1.5 ml tubes and washed twice with PBS. The DNA was extracted using proteinase K digest (100 μl of 25 mM Tris pH8.0, 100 mM NaCL, 1% SDS, 5 mM EDTA and 10 μg of Proteinase K followed by phenol/chloroform extraction and ethanol precipitation. The DNA was resuspended in 10 μl TE8 buffer (10 mM Tris, pH 8.0, 1 mM EDTA).

A partially random primer with the sequence GGGN$_6$ (50 ng) was added to 5 μl of DNA. 12 μl of a denaturing solution (50 mM KOH, 0.1 mM EDTA) was added to the DNA/random primer mix. After a five-minute incubation at room temperature, 12 μl of a neutralization solution (60 mM Tris (pH 7.5), 50 mM HCl) was added to neutralize the reaction. The DNA/primer mix was denatured at 94° C. for 5 minutes, incubated at room temperature for 10 minutes, and then placed on ice.

The amplification reaction was set up in a final volume of 30 μl. The following reagents were added to give the indicated final concentrations: (a) 1×NEB buffer 2 (1× NEB buffer 2: 50 mM NaCl, 10 mM Tris-HCl, pH 7.9, 10 mM $MgCl_2$, 1 mM dithiothreitol), 333 μM dATP, dCTP, dGTP, dTTP, 160 μM S-adenosylmethionine, and 10 ng/μl of bovine serum albumin (BSA) were combined and to which was added (b) DNA methyltransferase enzyme 1 (0.15 units/μl) (New England Biolabs) and incubated at 37° C. for 10 minutes, and followed by (c) adding Klenow polymerase to a final concentration of 0.167 units/μl, and Klenow exo- to a final concentration of 0.167 units/μl (New England Biolabs).

The reaction was incubated at 37° C. for 16 hours, and the reaction was stopped by the addition of EDTA to a final concentration of 5 mM, phenol/chloroform extracted, and ethanol precipitated. The DNA was resuspended in 40 μl of TE8 and 41 were separated on agarose gel to verify the presence of DNA.

The DNA was treated with sodium bisulfite and analyzed by methylation specific PCR as described in Example 1 using the GPR147 and RET assays. The presence of a band of the expected size for either marker indicated the methylation of the associated marker in the input DNA.

All references, including publications, patent applications, and patents, cited herein are hereby incorporated by reference to the same extent as if each reference were individually and specifically indicated to be incorporated by reference and were set forth in its entirety herein.

The use of the terms "a," "an," "the," and similar referents in the context of describing the invention (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to better illuminate the invention and does not pose a limitation on the scope of the invention unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the invention.

Preferred embodiments of this invention are described herein, including the best mode known to the inventors for carrying out the invention. It should be understood that the illustrated embodiments are exemplary only, and should not be taken as limiting the scope of the invention.

```
                          SEQUENCE LISTING


<160> NUMBER OF SEQ ID NOS: 232

<210> SEQ ID NO 1
<211> LENGTH: 1600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 1

gagtttattt tcgtttgcgt gcgatagggt ttttgtattt aagtgagtta aggaatgaat     60

ttcgaatttt tttgggaaag ttattaacgt ttttttcgta ttttttttag ggtttttgat    120

tacggagatt ttgtttgggg tataggtgtg ggagtcgtaa attttttttt gcgtcgtttt    180

ttttcgcgtg gaatgggacg gagtagtttt tttaggcgtt gtttggttgc ggaggggagc    240

gggtagcgag agtttcgggt tttcgtttgg gttttcgggt tttcggggcg ttggtttcgg    300

ttttcgcgta gcgtttagcg atttttgtcg gggttttcg gtagtcgcgt cgttattttt    360

cgttcggtta gcgcgggagg aaaaggggtt gcgttcggga gcgtcgagtt taggtttttt    420

tcggtggcgt gttcgcgttt cggggtgggg gtgtggtggg gaagagggag ggggcgaggt    480

taggggaggg tgcgaaggag gcgtttgttt ttaatttgcg ggcgggaggt gggtggttgc    540

ggggtaattg aaaaagagtc ggcgaggagt ttttcgaaat ttgttggaat ttcgggttcg    600

cgcggaggtt aggagttgag cggcggcggt tgtcggacga tgggagcgtg agtaggacgg    660

tgataatttt ttttcgatcg ggttgcgagg gcgtcgggta gaggttagga cgcgagtcgt    720

tagcggtggg atttatcgac gatttttcgg ggcgatagga gtagtttcga gagttagggc    780

gagcgttcgt tttaggtggt cggatcgttc gtcgcgttcg cgtcgcgttt tttgtaggta    840

acgggagacg ttttcgcgta gcgcgagcgt tttagcgcgg tcgttcgttt tttttttcga    900

gggataaatt ttttttaaat tcgattcgag tttttggatt aaattcgttt gcgtcgagag    960

tcgttcgcgt agagcgtttc gttttcggcg agatgttcga gcgtaaagaa ggtagaggta   1020

aagggaaggg taagaagaag gagcgaggtt tcggtaagaa gtcggagttc gcggcgggta   1080

gttagagttt aggtgggtgc gtagcgcggt tcgggtttta cgattttttt tttgtttttt   1140

ttattttttt ttttttttcgg atgtcgtggt tttttttttt tttttttttt cgttcgtttt   1200

tttcgttttg cgttttgagc gttcgttgag tcgcgcggtg tttttttttt tgggggtcgt   1260

cgtttatttg ggcgtcgagt tttatcgggc gtttacgttt agagtttagg gtaagggata   1320

gtagtttcgg tcgtattttt ttagagtttc gggagcgttt cgttttttgg tacggttttt   1380

ttttagcgtt ttagcggttg agtttagttc gggagtggga tttgggttat aggagtcgag   1440

gttgcgtgcg cgcgtgtttc gcgttataag cgttttgtac gggggtcgtg tgttttttag   1500

cgggaaacgt tggaatgggt cgtttggagg gagagtcggt tttttcggtg tgtttggtag   1560

cgtagaagtg ggtggtcgag taagaggtcg cgtgggaagt                         1600


<210> SEQ ID NO 2
<211> LENGTH: 1600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
```

```
<400> SEQUENCE: 2

atttttacg cggtttttg ttcgattatt tatttttgcg ttgttaggta tatcgagggg      60

atcggttttt tttttaggcg gtttatttta gcgtttttcg ttagagggta tacggttttc     120

gtgtaaagcg tttatggcgc ggggtacgcg cgtacgtagt ttcgattttt atagtttagg     180

ttttattttc gggttgggtt tagtcgttaa ggcgttgggg aggggtcgtg ttagggagcg     240

aagcgttttc gggattttgg gagggtgcgg tcgggattgt tgttttttgt tttgagtttt     300

gggcgtaggc gttcggtagg attcggcgtt taggtgagcg gcggttttta ggaggggaag     360

tatcgcgcga tttaacgggc gtttagagcg tagggcgaag aggacgggcg agggagaggg     420

ggagggagag gttacggtat tcgaggagga ggaggagtag gaggagtagg aggaggatcg     480

tggggttcgg gtcgcgttgc gtatttattt gggttttggt tgttcgtcgc ggatttcggt     540

tttttgtcgg agtttcgttt tttttttttg tttttttttt tgtttttgtt ttttttgcgt     600

tcggatattt cgtcggagac ggagcgtttt acgcggacgg ttttcggcgt aggcgagttt     660

ggtttaaggg ttcggatcgg gtttgggaaa agtttgtttt tcgaggggga gagcgagcgg     720

tcgcgttgag gcgttcgcgt tgcgcggggg cgtttttcgt tgtttgtagg gagcgcggcg     780

cggacgcggc gggcggttcg gttatttgga acgggcgttc gttttggttt tcggggttgt     840

ttttgtcgtt tcgggaagtc gtcgatgggt tttatcgttg gcggttcgcg ttttggtttt     900

tgttcggcgt tttcgtaatt cgatcgggga gaggttatta tcgttttgtt tacgttttta     960

tcgttcggta gtcgtcgtcg tttagttttt ggttttcgcg cgagttcgga gttttaataa    1020

gtttcgggga atttttcgtc ggtttttttt taattgtttc gtagttattt atttttcgtt    1080

cgtaggttgg aggtaggcgt tttttcgta ttttttttg gtttcgtttt tttttttttt     1140

tttattatat ttttatttcg aggcgcggat acgttatcgg gaggagtttg ggttcggcgt    1200

tttcgggcgt agtttttttt tttttcgcgt tggtcgggcg gggggtggcg gcgcggttgt    1260

cgggaatttt cgataggggt cgttggacgt tgcgcggaga tcgaggttag cgtttcggag    1320

attcgggaat ttaggcggag attcgaggtt ttcgttgttc gttttttttc gtagttaggt    1380

agcgtttggg agggttgttt cgttttattt tacgcggaaa aggacggcgt agagaaaagt    1440

ttgcgatttt tatatttgtg ttttaagtag agttttcgtg gttaggaatt ttgggagggg    1500

tgcgggggga acgttggtgg ttttttaga agagttcggg gtttattttt taatttattt     1560

aagtataaaa gttttgtcgt acgtaggcga aaataaattt                          1600


<210> SEQ ID NO 3
<211> LENGTH: 1350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

attttggcgt ttaatatcgt taatattagt gggttgttag gggtttcgtg ggaggcggtt      60

ttagtcgggg ttttgttggc gttggcggtg ttggttatcg tgggaggtaa tttgttggtt     120

atcgtggtta tcgtttggat ttcgagattt tagattatga ttaacgtgtt cgtgatttcg     180

ttggtcgtag tcgatttggt gatgggattt ttggtggtgt cgtcggcggt tattttggcg     240

ttgattggtt attggtcgtt gggcgttatt ggttgcgagt tgtggatttc ggtggacgtg     300

ttgtgtgtga tcgttagtat cgaaattttg tgcgttttgg tcgtggatcg ttatttggtt     360

gtgattaatt cgttgcgtta cggcgtattg gttattaagc gttgcgttcg gatagttgtg     420

gttttggtgt gggtcgtgtc ggtcgcggtg tcgtttgcgt ttattatgag ttagtggtgg     480
```

-continued

```
cgcgtagggg tcgacgtcga ggcgtagcgt tgttatttta attcgcgttg ttgtgttttc    540

gtttttaata tgttttacgt gttgttgttt tttttcgttt ttttttattt ttttttttttc    600

gtgatgtttt tcgtttacgc gcgggttttc gtggtggtta cgcgttagtt gcgtttgttg    660

cgcggggagt tgggtcgttt ttcgttcgag gagttttcgt cggcgtcgtc gcgtttttttg    720

gtttcggttt cggtggggac gtgcgtttcg ttcgaagggg tgttcgtttg cggtcggcgg    780

ttcgcgcgtt ttttgttttt tcgggaatat cgggtttttgt gtattttggg ttttattatg    840

ggtattttta tttttttgttg gttgtttttt tttttggtta acgtgttgcg cgttttgggg    900

ggtttttttt tagtttcggg ttcggttttt tttgttttga attggttagg ttatgttaat    960

tttgttttta attcgtttat ttattgtcgt agttcggatt ttcgtagcgt ttttcgtcgt   1020

tttttgtgtc gttgcggtcg tcgtttgttt tcggagtttt gcgtcgtcgt tcgttcggtt   1080

tttttttttt cgggcgtttt tgcggttcgg agtagtttag cgtagtttag gttttgttaa   1140

cggttcgacg ggtaggtaat cggggtagag ggatcggcgg tttagggtcg ggaagtatgc   1200

gatgtgttcg tgggttaatt ttttgagtgt ggagtttatt aagagaaggt gggatggttt   1260

tgtttggaga gaaaagggaa cgaggagtag cgaattaaaa tgggatttag ggtttttttt   1320

ttttcggatt tagttattag ggtagaagta                                    1350


<210> SEQ ID NO 4
<211> LENGTH: 1350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

tgtttttatt ttagtgattg gattcggaaa gaaaaggatt ttgggtttta ttttggttcg     60

ttatttttcg tttttttttt tttttaagta aagttatttt attttttttt aataaatttt    120

atatttaaaa agttgattta cggatatatc gtatgttttt cgattttgag tcgtcggttt    180

ttttgtttcg gttatttatt cgtcgagtcg ttggtaaagt ttgggttgcg ttgggttgtt    240

tcgggtcgta ggaacgttcg aggggaagag ggtcgggcgg gcggcggcgt agggtttcgg    300

aggtaggcga cggtcgtagc ggtatagaag acggcggaag gcgttgcgaa agttcgggtt    360

gcggtagtag atgagcgggt tgaaggtaga attggtataa tttagttagt ttagggtaag    420

gaaagtcggg ttcgggatta gagaggggtt ttttagggcg cgtagtacgt tggttagaaa    480

gaagggtaat tagtagagag tgaaggtgtt tatgatgaga tttaaggtgt atagggttcg    540

gtgttttcgg agaggtagga ggcgcgcggg tcgtcggtcg taggcgggta tttttttcggg    600

cggagcgtac gtttttatcg gggtcggggt tagagagcgc gacggcgtcg gcggagattt    660

ttcgggcgga aagcggttta gtttttcgcg tagtaagcgt agttggcgcg tagttattac    720

gaaaattcgc gcgtagacga agagtattac gagaagagga aggtagaagg agacggagga    780

ggatagtagt acgtagggta tgttggaggc gaaggtatag tagcgcgggt tggagtggta    840

gcgttgcgtt tcggcgtcgg tttttacgcg ttattattgg tttatgatgg gcgtaaacga    900

tatcgcggtc gatacgattt atattaggat tatagttgtt cgggcgtagc gtttggtgat    960

tagtgcgtcg taacgtagcg ggttggttat agttaggtag cggtttacgg ttagggcgta   1020

tagggtttcg atgttggcgg ttatatatag tacgtttatc gaggtttata gttcgtagtt   1080

agtggcgttt aacggttagt ggttagttag cgttaaggtg gtcgtcggcg gtattattag   1140

gagttttatt attaggtcgg ttgcggttag cgaagttacg aatacgttgg ttatggtttg   1200

gagtttcgga gtttaggcga tggttacgat gattagtagg ttgtttttta cggtggttag   1260
```

tatcgttagc gttagtaggg tttcggttag ggtcgttttt tacggaattt ttggtagttt 1320

attggtgttg gcggtattgg gcgttagggt 1350

<210> SEQ ID NO 5
<211> LENGTH: 1600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

cgaaaagttt ttgaggcgtt gcgtgtattt tattttagga tatcgtgtgt gcgcgtcgag 60

ttgagtgcga ggaacgtggc gcgagggtcg gggatgtcg ggttgcgtgg gtgtgagttt 120

tcgcgcgatc gcgatttcgc gtttttttcg ttttcgtcgg aacgtgatcg tagtcgtatt 180

ttttttttag ttttttttta gttagacgtt tttttttagg tttttttggg cgtttattgt 240

aaattttgcg attaaaatac gtcggtgagt tcggtttatc gatagatgga ttaatcgttt 300

ttttttcggt taggggagga ggaatttttt aatttcggag tttagggagt cgggagttgt 360

ttcgggacga gtttttcgga gtttagtcgg ttgcggagtt tcggttcggg tcggtttcgg 420

ggtttttttg tcggggtggg gtgcgagttt ttgttcgatt tttttggggc ggtttaggta 480

ggtttgtcgg ttttcgagga ggtggttagg gcgttttggt ttagtaggtt ttttttcgag 540

tcggggggag gggagatcgg ttggggaagg ggtatttcga aggggtggag gtcggggcgg 600

gcgggaggta agcgcgtcgc gggcgtgagg gtaaagtttt cgaggttcgc gcggagagta 660

tacgtgtatg tgcgcgcggg gttaggtcgg ggtcggtagg atgcgttggg ttcgggggcg 720

cgcggggtcg gcgtcgaagg ggataatttt tttttttggt attatcgggg agacgttttg 780

tcggtttcgg tttttgggcg tagggacgtt ttagtttacg gagggtggag ttttttttag 840

attcgggtta tcggttgggg tttttttaac gttttgtttt tcgagttttc ggatggttcg 900

ggttttacgg atttcgcgtt ttttagtttt agtttagttt tttaggtttt ttagatttag 960

cggcgtaggg ggcgggggta ggggtagtgg gggttggagg gcgtagtcgg tttttagggt 1020

ggggagagtt gcggggggag gaggaggagg gtgtcgacgt ttgagtgggt tcgagttcga 1080

gtcgtagtcg ggggagttag ttagttttcg gttaaggtag taggttagtt ttaggaaggg 1140

cgggcgattg agtcgaggga gtcggcggtt gggttttttt ttcggttcgc gattttcggc 1200

gtcgtcgtcg tcgttatcgt tatcgttatc gttttcgttt tgtcgtcgtc gtcgttgtag 1260

agtatcgtag tttcgtcgcg ttttcgcgtt tcgcgtttcg cgtcgttagt cgtttgggag 1320

ttcgagcgtc gagttcgggg cggaggagag gggcgttggc gcgagagttc gggcgaggga 1380

gtcgcgaagg gagaaggggg cgggcggagg gaggagtagg gagagtggga gaagggggag 1440

ggagagagga gagcgaggga gagttggaga gagcgagagt aaagagcgag cgagggagag 1500

gagagagaga gagaggagag agaaagatat acgtacgtag agatatacgg ttattggaat 1560

tttattagaa aaaagtgagt cgagtaaggg ttagcgggag 1600

<210> SEQ ID NO 6
<211> LENGTH: 1545
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

ttttcgttaa tttttgttcg gtttattttt ttttaatgga attttagtga tcgtgtgttt 60

ttgcgtgcgt gtgttttttt tttttttttt tttttttttt ttttttttcg ttcgtttttt 120

gttttcgttt tttttagttt tttttcgttt tttttttttt gcggtttttt cgttcgggtt 180

-continued

ttcgcgttag cgtttttttt tttcgtttcg ggttcggcgt tcgggttttt aggcggttgg 240

cggcgcgggg cgcggggcgc gggagcgcgg cggagttacg atgttttgta gcggcggcgg 300

cgataaggcg aaggcggtgg cggtggcggt ggcggcggcg gcggcgtcgg ggatcgcggg 360

tcgagaggag agtttagtcg tcggtttttt cggtttaatc gttcgttttt tttgggattg 420

atttgttgtt ttggtcggaa attgattggt tttttcggtt acggttcggg ttcgaattta 480

tttaagcgtc ggtatttttt tttttttttt ttcgtagttt tttttatttt ggggatcggt 540

tgcgtttttt aatttttatt gtttttgttt tcgtttttttg cgtcgttggg tttgggaagt 600

ttggggagtt gagttgaggt tggagggcgc ggagttcgtg gggttcgagt tattcggggg 660

ttcggggggt agggcgttag aaaaatttta gtcggtggtt cgggtttgag gggggtttta 720

tttttcgtgg gttaaggcgt ttttgcgttt aggagtcgag gtcgataaag cgtttttttcg 780

atggtgttag ggaaaggaat tatttttttc ggcgtcggtt tcgcgcgttt tcgaatttaa 840

cgtattttgt cggtttcggt ttagtttcgc gcgtatatat acgtgtgttt ttcgcgcgga 900

tttcgggaat tttgttttta cgttcgcggc gcgtttgttt ttcgttcgtt tcggttttta 960

ttttttcgag atgttttttt tttagtcggt tttttttttt ttcggttcgg gaagaagttt 1020

gttgggttag ggcgttttga ttatttttttc ggaggtcggt aaatttgttt gaatcgtttt 1080

agaggaatcg ggtaggggtt cgtattttat ttcggtagga gggtttcgag atcgattcgg 1140

gtcggggttt cgtagtcggt tgggtttcga ggagttcgtt tcgaggtagt tttcggtttt 1200

ttaggtttcg gggttggggg gttttttttt ttttagtcgg gaagggggcg attgatttat 1260

ttgtcggtgg gtcgggttta tcggcgtgtt ttagtcgtag aatttataat aaacgtttag 1320

aaggatttaa aaggaagcgt ttggttggga aagggttgga ggagaggtgc ggttgcggtt 1380

acgtttcggc gagagcggga gaggcgcggg gtcgcggtcg cgcgagggtt tatatttacg 1440

tagttcggta tttttcggtt ttcgcgttac gtttttcgta tttagttcgg cgcgtatata 1500

cggtgttttg gggtggggta tacgtagcgt tttagaaatt tttcg 1545

<210> SEQ ID NO 7
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

gaggtattag tttttgaagg tttatttttt aatattggtt gcgagagtaa gaatggtgtg 60

taatttataa aagtcgttat tgttgtaggt aagttgtagt aaacgattcg cgttcgagta 120

ttttcgtttt cgttttcgtt gcggtttcgt ttacgacgat tttggggaat tataagtttc 180

gttatatagc ggggagcgtt cggagttcgc gtcggtttcg tttttagttc ggtttttatt 240

ttcggtttcg ttttcggttt tttttcgtcg ggttaatttc gaagagtcgt cggtggtcgc 300

ggtagacgga agtcgaacga gtttttcggc ggttgtagga tgggggattt taaagtgaaa 360

gtggcggtgc ggatacgatt tatgaatcgg cgaggtgaga gtcgagtttt tttgggtcgt 420

cggggcggag gcggtaggtg tttggcgcgt tttttttcg gtcgtcgtgg ggggttcggc 480

ggtttcgttt ttatagttag cggcggggcg cgaggagggg ttcggggatt ttgaaattcg 540

ttttcgcgtt gagacgttcg gttttttttt tttttttttt tttttttttg gttagtttcg 600

tttttggcgt cgtcgggttt ttcgtgtcgg tttcgttgtt tttttcgttt gcgttcgttt 660

cgtttttgcg ttttttttgtt ttttcgtttt tttcggaggt tttcgagggc gttttcggtt 720

ttcgcgttta gtttcgtttt ggttttttag tttcgttttt ttttcgttag ttgttatcgt 780

-continued

```
cgttttcgcg cgcgggtcgt tagtttttgt agttcgtttc gggatcgttc gggatttttc    840

gggatttcgc gtttcgttcg ggtcgtttaa gtttgtatcg ttttggttcg cggcgggaag    900

aagggtaggg ggttaggcgg gtgtttcgcg gcgagttttt tttatttggg cgttttgaga    960

ttggggttag gtggaggaga tgttttttc gttgtttttg gatagttgag aaagttttgg   1020

ttttgtttga agttttattt attatttttt aataaatagt taaagtgtta agatttttgt   1080

ggaattgtat tttttgata                                               1100
```

```
<210> SEQ ID NO 8
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

tgttagaaag atataatttt ataagaattt tggtatttta gttatttatt gagagatgat     60

gaatgagatt ttaggtaaaa ttaaaatttt tttaattgtt taaaaataac gaaaagggta    120

ttttttttat ttgattttaa ttttaggacg tttaggtgga aggaattcgt cgcggggtat    180

tcgtttggtt ttttgttttt tttttcgtcg cgggttaagg cggtgtaggt ttgggcgatt    240

cgggcgagac gcggggtttc ggggggtttc gggcggtttc gaggcgggtt gtaggggttg    300

gcgattcgcg cgcgggggcg acgatgatag ttggcgggga aggagcgagg ttgaggggtt    360

aggacgaggt tgggcgcgag ggtcgagggc gttttcggga attttcgggg gagacgagag    420

ggtaaaaggg cgtaggggcg gggcgggcgt aggcggaagg ggtagcgggg tcggtacgag    480

gggttcgacg gcgttaggga cggggttggt tagggggggaa gggaggggag aagagggagt    540

cgggcgtttt agcgcgggag cgggttttag ggttttcggg tttttttttcg cgtttcgtcg    600

ttgattatag gggcggggtc gtcggatttt ttacggcggt cgagggaagg gcgcgttagg    660

tatttgtcgt tttcgtttcg gcggtttagg agggttcggt ttttatttcg tcggtttatg    720

ggtcgtattc gtatcgttat ttttattttg gagtttttta ttttgtagtc gtcgaggaat    780

tcgttcggtt ttcgtttgtc gcggttatcg gcgatttttc ggggttgatt cggcgggagg    840

gggtcggggg cggagtcggg ggtggggatc gggttggggg cggggtcggc gcgagtttcg    900

ggcgtttttc gttgtatggc gggatttgta gtttttttagg gtcgtcgtgg gcggggtcgt    960

agcgaaggcg gggggcgggaa tgttcgggcg cgagtcgttt gttataattt atttatagta   1020

atgacggttt ttgtaaatta tatattattt ttgttttcgt agttagtatt gagaagtaag   1080

tttttaagag ttgatatttt                                              1100
```

```
<210> SEQ ID NO 9
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

ttgtggagcg gaggagggga ggtttggggt cgcggcggtg tgcgtttcgt tttgatcgta     60

gagtttttttt ttcgaggaaa gcggttggtt cggtttcggt tggtgattac gcggggtttt    120

tgtttgtttg gtgcgtaggt gagggtttgt tttttcgttg cgtttcggat agtttggagg    180

tgagtacgcg ttgggttttg gatcgcgagt agcgggagaa gtacgagttg gtggtcgtgt    240

gtatcgtgta cgtcggcgcg cgcgaggagg tggtgatggt gttttttttcg gtgatcgtgt    300

acgacgagga cgattcggcg tttatttttt tcgcgggcgt cgatatcgtt agcgtcgtgg    360

tggagtttaa gcggaaggag gtgtttgttc gcgcgtgttg tggtttattt agtgtttgtt    420
```

-continued

ttcggttata gttcgttttt cggtcggttt agtgttcgtg tagttattta atcgtgtggt 480

cgattattcg cgtttttatt tgtttttcgt tttcgtttgc gtcgtttgtt ttagggggag 540

gggaaggggg agttttgtta gtatttagtt gggttttgtt tcgggaggta aggattagga 600

cgaggttcga gggttcgcgt ttggggtata tttgtgtcgt tgtaggcggg cgcggcgcgt 660

tgttcgggcg gggagtattt gtcgggaggg tattttttt tattagtagt tagtttttaa 720

cgggagggtt tttgagtgat tacgagtaga gtcggggatt ggagaaggac gggaaggcgg 780

attattttcg gcgtcgttcg tttcgttttt tttcggttcg cgttggtgga gcgcgatcgt 840

tatttgttgg 850

<210> SEQ ID NO 10
<211> LENGTH: 798
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

ttagtaggtg gcggtcgcgt tttattagcg cgagtcggag aagggcgggg cgggcggcgt 60

cggaggtgat tcgtttttc gttttttttt aattttcggt tttgttcgtg gttatttaag 120

ggtttttcg ttggggttta attgttggtg ggagggagtg ttttttcggt agatgttttt 180

cgttcgggta gcgcgtcgcg ttcgtttgta gcggtataag tatgttttag acgcgagttt 240

tcgggtttcg ttttgttttt ttttttagga tagacggcgt agacggaggc gaaggataaa 300

tgaaagcgcg aatggtcggt tatacggttg ggtggttata cggatattaa atcgatcgag 360

aaacgaattg tggtcggaga tagatattgg gtagattata gtacgcgcgg ataagtattt 420

tttttcgttt gaattttatt acggcgttgg cggtgtcgac gttcgcgggg aaggtgggcg 480

tcgagtcgtt ttcgtcgtat acggttatcg ggaagggtat tattattatt ttttcgcgcg 540

cgtcggcgtg tacggtgtat acggttatta gttcgtattt ttttcgttgt tcgcggttta 600

gggtttagcg cgtgtttatt tttaggttgt tcggggcgta gcggaagggt agatttttat 660

ttgcgtatta agtagatagg ggtttcgcgt gattattagt cgggatcggg ttagtcgttt 720

ttttcgggaa gggggttttg cggttagagc ggggcgtata tcgtcgcggt tttaggtttt 780

ttttttttcg ttttatag 798

<210> SEQ ID NO 11
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

atcgtttttt cgtaggggtt ttaggattta tttagatttc gtttgttttt tttttcgcgg 60

taggtttcgt tgtatcgtgt atttttttcg cgagaagttg attttgcgga aggcgttcgt 120

tattatcgtc gttatttggg ttttggcgtt gtttattatg tgtttttcgg tcgttacgtt 180

gatcgttatt cgtgaggagt attattttat ggtggacgtt cgtaatcgtt tttattcgtt 240

ttatttttgt tgggaggttt ggttcgagaa gggtatgcgt agggtttata ttattgtgtt 300

tttttcgtat atttatttgg cgtcgttggc gtttatcgtg gttatgtacg ttcgtatcgc 360

gcgtaagttt tgttaggttt cgggttcggt tttcgggggc gaggaggttg cggattcgcg 420

agtatcgcgg cgtagagcgc gcgtggtgta tatgttggtt atggtggcgt tgttttttac 480

gttgttttgg ttgtcgtttt gggcgttgtt gttgtttatc gattacgggt agtttagcgc 540

gtcgtagttg tatttggtta tcgtttacgt ttttttttc gcgtattggt tggttttttt 600

-continued

taatagtagc gttaatttta ttatttacgg ttattttaac gagaattttc gtcgcggttt 660

ttaggtcgtt tttcgcgttc gtttttgttc gcgttcgtcg gggagttata aggaggttta 720

tttcgagcgg ttcggcgggt ttttgtatag gcgggttttc gtggtggtgc ggtttagcga 780

tttcgggttg ttttttgagt cgggttttag tagtggggtt tttaggttcg gtcgtttttc 840

gttgcggaat 850

<210> SEQ ID NO 12
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

atttcgtagc gggaggcggt cgggtttggg ggttttattg ttagggttcg atttagaggg 60

tagttcggag tcgttgggtc gtattattac gaagattcgt ttgtgtagaa gttcgtcggg 120

tcgttcggag taggtttttt tgtggttttt cgacgggcgc gggtagaggc gggcgcggaa 180

ggcggtttgg aagtcgcggc ggaagttttc gttgaagtag tcgtagatga tggggttggc 240

gttgttgttg aagaaggtta gttagtgcgc gaaggggaag gcgtagacgg tgattaggtg 300

tagttgcggc gcgttgagtt gttcgtagtc gatgagtagt agtagcgttt agagcggtag 360

ttaggatagc gtgaagaata gcgttattat gattagtatg tgtattacgc gcgttttgcg 420

tcgcgatgtt cgcgggttcg tagtttttc gttttcgggg gtcgggttcg gggtttggta 480

gagtttgcgc gcgatgcggg cgtatatgat tacgatgagc gttagcggcg ttaggtagat 540

gtgcgagaag agtatagtgg tgtagatttt gcgtatgttt ttttcgggtt aggtttttta 600

gtaggagtag agcgggtagg agcggttgcg ggcgtttatt atgaagtggt gtttttttacg 660

ggtgacggtt agcgtgacgg tcgagggata tatgatgagt agcgttaggg tttagatgac 720

ggcgatggtg acgagcgttt ttcgtagggt tagtttttcg cggaaagggt gtacgatgta 780

gcggaatttg tcgcggggag agagataggc gggatttggg tgggttttag ggtttttgcg 840

aggggacggt 850

<210> SEQ ID NO 13
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

tttagtttcg gaatcgcgga ttgcgtttag tgacggattt aaatttattt ttttttttga 60

tttcgtcgta ggatgacgtt ttaattttcg ggtgcgttta ttgtttaagt gattcgtgag 120

acggagcggt tttttttag agtttcggaa gacgaagtga tttgttttac gttcgtttcg 180

tttagtttta ttcgtatacg gggaattgc gtagaggcgg aagagggagg ttgtcgaggg 240

gtttcgagga agtttcgggt acggcgcggg ggacgtagtc ggtttaagag cgagttggta 300

ttgagtaagt agcgacggag tcggcgaaag aaggttaacg atcgcgagcg taatcgaatg 360

tataatttta attcggtatt ggacgttttg cgcggtgttt tgtttatttt tttagacgac 420

gcgaagttta ttaagatcga gacgttgcgt ttcgtttata attatatttg ggcgttgatt 480

taaacgttgc gtatagcgga ttatagtttg tacgcgttgg agtcgtcggc gtcgtattgc 540

ggggagttgg gtagtttagg cggtttttc ggggattggg ggttttttta tttttagtt 600

<210> SEQ ID NO 14
<211> LENGTH: 600
<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

gattggggag tagagggatt tttagttttc gggggaatcg tttgggttgt ttagtttttc 60

gtagtgcggc gtcggcggtt ttagcgcgta taagttgtgg ttcgttatgc gtagcgtttg 120

agttagcgtt tagatgtagt tgtgggcgaa gcgtagcgtt tcgattttgg tgagtttcgc 180

gtcgtttggg aaggtgggta ggatatcgcg tagggcgttt agtgtcgagt tgaggttgtg 240

tattcgattg cgttcgcggt cgttggtttt ttttcgtcga tttcgtcgtt gtttgtttag 300

tgttaattcg tttttaggtc ggttgcgttt ttcgcgtcgt gttcggagtt ttttcggggt 360

ttttcggtag tttttttttt tcgtttttgc gtagtttttt cgtgtgcgag tggggttggg 420

cggggcggac gtggggtagg ttatttcgtt tttcgaggtt ttggggaagg atcgtttcgt 480

tttacgggtt atttggatag tgggcgtatt cgagggttga ggcgttattt tacggcgggg 540

ttagagggaa gggtaagttt gagttcgtta ttgggcgtag ttcgcgattt cgaggttagg 600

<210> SEQ ID NO 15
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

ttagtttcgg tcgtattgta tagcgaggtc ggttcggagt tcggatgttg ggttcggttt 60

cgtcgaggtt cggtttggtt gtaaagtaga ggggggcgag ggaagtcggg ttagcgggtg 120

tcgcgggtag tcggcgttcg ggacggggtg tggcgtttag agcgttgttg tttttcgtag 180

ttaggaggtt ggatgtcggg tttgggtgtt ttttagaagg agtcgtatta gcgacgaggg 240

aagaggaatt ggtttttcgg gtagtttttt tcgttttaaa tttttttttt tcgcggaggg 300

tgggcgggcg gagggaggaa gcgtagtcgg ggaacgtggc gttcgcgttt ttttcgttcg 360

ggggttgcgg ttgggttgag tgtgttttta aatttgagtt tttcgttttt cgcggtgggg 420

tcgggattcg cggttcgggc gggggcgggc gcggtgattg gcggtcgggt cgggttcgtt 480

tttcggcgtt gggtagcggg gcgttgggga gtagcgcggc gcgtacgggt cggggcgcgt 540

aggtttcgtc gtcggtgagt acgggttttt tttcgcgtgg tttcgtcggg ttcgtttggt 600

ttgtttattt tcggagttat ttttgttttc gtatgggttg gcgaagttgg gaggagcgag 660

ttggagttag agcgcgcgtc gggcgcgttt cgtcgttgtt tgattcggcg ttcgtagttc 720

gggcgtagta cgtcggtcgt aggagtacgg atgtttttcg gagtcgcggg ttggtaggta 780

tcgaagtgtt ttgttttggg gttggcgagg ggagggtaaa tttggaattt ttcgggtatt 840

ttttagttcg 850

<210> SEQ ID NO 16
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

cgggttgggg ggtgttcggg ggattttaga tttgtttttt tttcgttagt tttagggtag 60

gatatttcgg tatttgttag ttcgcggttt cggggggtat tcgtgttttt gcggtcggcg 120

tgttgcgttc gaattgcggg cgtcgagtta ggtagcgacg gggcgcgttc ggcgcgcgtt 180

ttggttttag ttcgtttttt ttaatttcgt tagtttatgc gggggtagag gtggtttcgg 240

aggtgggtag gttaggcgga ttcggcgagg ttacgcgaga gggagttcgt gtttatcggc 300

-continued

```
gacgggattt gcgcgtttcg gttcgtgcgc gtcgcgttgt tttttagcgt ttcgttattt    360

aacgtcgagg ggcggattcg attcggtcgt taattatcgc gttcgttttc gttcggatcg    420

cgagtttcgg ttttatcgcg aggggcgggg ggtttagatt taaagatata tttagtttag    480

tcgtagtttt cgggcgggag gaacgcgggc gttacgtttt tcggttgcgt tttttttttt    540

cgttcgttta tttttcgcga ggaggaaaag tttggggcgg gggagattgt tcgggaagtt    600

agtttttttt ttttcgtcgt tagtgcggtt ttttttggaa gatatttaaa ttcgatattt    660

agtttttggg ttgcgagagg tagtagcgtt ttgggcgtta tatttcgttt cggacgtcgg    720

ttattcgcga tattcgttgg ttcggttttt ttcgtttttt tttgttttat agttaggtcg    780

agtttcggcg ggatcgagtt tagtattcgg gtttcgggtc ggtttcgttg tgtagtgcgg    840

tcggagttgg                                                           850


<210> SEQ ID NO 17
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

ttttgtatag gagtagtgat tttagtattt atttaatttt ttttcggcgt cgagtttagt     60

tggagaggtt aggggtggta gtgattggta ggaggtcggg gcggggggaa tttttaagtt    120

cggcgtttgg ggttgcgggt tcgattcgag attcgttttt tttgtaagtt tcgagtcgtt    180

ggttaggttc gttattgcgt attagtcgta ttcgcgagcg ttggttttgt cggtttgagt    240

tagggtgggt agggtcggga tttacggcgg aggtggggtc gggtcgagta gtttcggggg    300

attttcgaag ttatagcgtt ttgttttttt gtacgtttcg cgttttcggt tttcgattgg    360

ttgtcgggtt tagagttcgt ttagaattgg atcgttcgtt tgtcgttcgg gtttggtttt    420

atttttagag ggagtttaga atttggtcgt agtttttaga gattattttt atttcgtggt    480

ttgcgtcgaa gttgggcgga ggatagtggg tggttaggtt ttttcgggtt agaattcggg    540

atttttgtta gttattcgtg ttaggataga tttaagtttt taaaacgcgg atggatgtat    600


<210> SEQ ID NO 18
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

gtatatttat tcgcgttttg ggggtttgag tttgttttgg tacgggtagt tggtaggggt     60

ttcgagtttt ggttcggaag ggtttggtta tttattgttt ttcgtttaat ttcggcgtag    120

gttacggggt gagggtagtt tttaaaaatt gcgattaggt tttaggtttt ttttgggggt    180

ggagttagat tcgagcgata agcgaacggt ttaattttgg gcgggtttta ggttcgatag    240

ttaatcggag gtcgggggcg cggagcgtgt agggaggtaa ggcgttgtag tttcggggat    300

ttttcgaggt tgttcggttc ggttttattt tcgtcgtggg tttcggtttt atttatttta    360

gtttaggtcg gtagagttag cgttcgcgga tgcggttggt gcgtagtagc gggtttggtt    420

agcggttcgg ggtttgtagg gagggcggat ttcgggtcgg attcgtagtt ttagacgtcg    480

ggtttggggg ttttttttcgt ttcggttttt tgttagttat tattattttt agttttttta    540

attgagttcg gcgtcgggag aggattaagt aagtgttgag gttattgttt ttgtgtaaga    600


<210> SEQ ID NO 19
<211> LENGTH: 1548
<212> TYPE: DNA
```

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

aggtagggat aaagtgtaag aggtaaaatt ggttgaaaag tagaagtgta ggagtcgtta 60

aggggcggga cgaataggtt cgtgggtcgg gcggagttaa gggtggggt cggggttttt 120

ttaggtggta ttcgcggcgt tagtttttaa acgttatagc gtttcgggcg tttaggagaa 180

cgcgaacggt ttttcgcggg agcgggcgag taggaggggg cgtcgggtta tatatatagc 240

ggttcggttt cgggcgggtt tggcgtttag ggaggcgcgt attgtttttt agagttttag 300

ttttagtcgc gcgtttttcg ttcggttcgt cgttttatgt agtcggggta gagttcggcg 360

ttcgggggtt tcgtcgtttg tttttcgtat tttttcggtt gcgtattttt gttcgaggtc 420

ggtcgtgcgt tttcgcggga cgttataggc gtagttttgt tttttagttt ttcgggcgta 480

ttgatcgttt gatcgacgta cggttttcgg gtcgggatgt cggggttcgg gacggtcgcg 540

gtagcgttgt tttcggcggt tttgttggtt ttgttggcgt tttgggcggg tcgagggggc 600

gtcgtcgtat ttattgtatt taacggtacg ttggaggtcg agttggagcg tcgttgggag 660

agtttggtgg cgttttcgtt ggcgcgtttg tcggtggtag cgtagtttaa ggaggcggtc 720

gtttagagcg gcgtcggcga ttatttgttg ggtattaagc ggttgcggcg gttttattgt 780

aacgtgggta tcggttttta tttttaggcg tttttcgacg gtcgtatcgg cggcgcgtac 840

gcggatattc gcgatagtga gtggcgcggt taggcgcgaa ggggcggggg cggggggtaa 900

cggtcgtcgg gttaattcgt ttagttatat tttgagattt tcggcgggta tttgttcggg 960

ggtttcggga atcggggcgg attcgggttt cggttttttt tgacgcgggg ttggggacgt 1020

agatattttt ggtttcggta gtttagcgta atttttgagg tcgggcgtcg tttttcgttt 1080

ttagaaattc gggtttcgag cgtcgaattt tagcgttttc gttcgtgggt atagggcgcg 1140

cggtgtagtt ataggggggtt cgagatacgc gtttcggttt ggtttaggtt ggggaatcgt 1200

tggggtcggg ttcgcgtttg aaggttcggg attgggtgcg gtcgtcgggg gtttttttata 1260

taggtaagtt aatttgagtt agcgtaggtt tgggtttcgg aggttttaga gggtagtttg 1320

ggttttggag gtttttgggg gcggttgcgt cgggaatttt ggtttttttat ttttaatttt 1380

attttagaaa tagggttttc ggaggcgaat aagtcgaggg gcggagtggg ttagggatta 1440

tttgtttcgt aatgatttgc gtttcgtttt taggtttgtt ggagttttcg ttcgtggagc 1500

ggggcgtggt gagtattttc ggcgtggtta gtcggttttt cgtggtta 1548

<210> SEQ ID NO 20
<211> LENGTH: 1600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

tggttacgaa gaatcggttg gttacgtcga agatgtttat tacgtttcgt tttacgggcg 60

agagttttag taggtttggg ggcggggcgt aggttattgc ggggtaggtg atttttggtt 120

tatttcgttt ttcggtttgt tcgttttcgg ggattttatt tttggggtgg ggttggggat 180

aaagggttag ggttttcggc gtagtcgttt ttaagggttt ttagagttta agttgttttt 240

tagggttttc ggagtttaag tttgcgttag tttagattag tttgtttgtg taggggattt 300

tcggcggtcg tatttagttt cggattttta gacgcgagtt cgattttagc ggttttttag 360

tttgggttag gtcggggcgc gtgtttcggg tttttttgtgg ttgtatcgcg cgttttgtgt 420

ttacgggcga aggcgttgga attcggcgtt cggagttcga gtttttgaag gcgggaggcg 480

-continued

gcgttcgatt ttaggggttg cgttgggttg tcggagttaa gagtgtttgc gtttttagtt 540

tcgcgttaga agggatcgga gttcgagttc gtttcggttt tcggggtttt cgagtaggtg 600

ttcgtcgagg gttttagagt gtgattgagc gggttggttc ggcggtcgtt gtttttcgtt 660

ttcgtttttt cgcgtttggt cgcgttattt attgtcgcgg gtgttcgcgt gcgcgtcgtc 720

gatgcggtcg tcggggagcg tttggaggtg gaagtcgatg tttacgttgt agtagagtcg 780

tcgtagtcgt ttgatgttta gtaggtagtc gtcggcgtcg ttttggacgg tcgttttttt 840

gggttgcgtt gttatcggta ggcgcgttaa cgagagcgtt attaggtttt tttagcggcg 900

ttttagttcg gtttttagcg tgtcgttggg tgtagtgggt gcggcggcgt tttttcggtt 960

cgtttagggc gttagtaagg ttagtaggat cgtcgggagt agcgttatcg cggtcgtttc 1020

gggtttcgat atttcggttc gagggtcgtg cgtcggttag gcggttagtg cgttcgggaa 1080

gttggggggt agagttgcgt ttgtggcgtt tcgcgggagc gtacggtcga tttcgggtag 1140

gagtgcgtaa tcgaggaggt gcgggaggta agcgacgggg ttttcgggcg tcgggtttta 1200

tttcggttgt atggagcggc gagtcgggcg gaaagcgcgc ggttggagtt gggattttga 1260

ggagtagtgc gcgttttttt gagcgttagg ttcgttcgag gtcgagtcgt tatatatata 1320

gttcggcgtt ttttttatt cgttcgtttt cgcgggggt cgttcgcgtt tttttgggcg 1380

ttcggggcgt tgtggcgttc gcggttggtc gtaggtcgtt tgttaattag ggtcggggga 1440

agggaggagg ttggggatta gcgtcgcgag tgttatttgg agggatttcg gtttttattt 1500

ttggtttcgt tcggtttacg gatttgttcg tttcgttttt tggcggtttt tatatttttg 1560

tttttagtt agttttgttt tttgtatttt gtttttgttt 1600

<210> SEQ ID NO 21
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

agggtgaagt ttgagagttt aaatggttaa ttttataggg ttgaacgttt tagaagtcgt 60

aggttcgttg gggttgattt tggtagttgt cgtggaggtg gggtattgt tgggtaacgg 120

cgcgttgttg gtcgtggtgt tgcgtacgtc gggattgcgc gacgcgtttt atttggcgta 180

tttgtgcgtc gtggatttgt tggcggtcgt ttttattatg tcgttgggtt tgttggtcgt 240

atcgtcgttc gggttgggtc gcgtgcgttt gggtttcgcg ttatgtcgcg tcgttcgttt 300

ttttttcgtc gttttgttgt cggtttgtac gttcggggtg gtcgtatttg gtttggtacg 360

ttatcgtttt atcgtgtatt cgttgcggtt aggttcgcgg tcgtcgtttg tgttcgtgtt 420

tatcgtcgtg tgggtcgcgg cgggattgtt gggcgcgttt tttttgttcg gtacgtcgtt 480

cgtatcgttt tttgtttttg ttcgttgttc ggttttggtt gggggtttcg ggtttttttcg 540

gtcgttttgg gttttgttgg ttttcgcgtt gttcgttttt ttgttgttcg gcgtttacgg 600

cggtattttc gtggtggcgc gtcgcgttgt tttgaggttt ttacggtcgg cgcgcgggtt 660

tcgattttat tcggattttt tggatagtcg ttttttatt ttgtcgtcgt ttcggtttcg 720

tttgttcggg ggtaaggcgg ttttggtttt agcgttggtc gtgggttaat ttgtagtttg 780

ttggttgttt tatggttgcg cgtgtttggc gttcgtagcg cgggtcgcgg aagtcgaagc 840

ggttgttatt tgggtcgttt attcggtttt cgcggtttat ttttttttgt acgggttgtt 900

gtagcgtttc gtgcgtttgg tattgggtcg tttttttcgt cgtgtattgt ttggatttgt 960

gcgggtttgt atttcgtaag tttggtattc gcgggtattt ttgtaatgtt tttagagatt 1020

-continued

tttagagggt tttgtcgtag gttttttga ggttttagaa tagattttcg agttggtagg 1080

agggcggagt ttcgtatatt 1100

<210> SEQ ID NO 22
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

ggtatgcggg gtttcgtttt tttgttaatt cgggggtttg ttttggagtt ttagaagggt 60

ttacggtagg gtttttggg ggtttttgga ggtattgtaa gagtgttcgc gggtgttagg 120

tttgcggagt gtaggttcgt ataggtttag gtagtgtacg gcgagagagg cggtttagtg 180

ttaagcgtac ggggcgttgt agtagttcgt ataggaaggg gtgagtcgcg aaggtcgagt 240

aggcgattta ggtgatagtc gtttcggttt tcgcggttcg cgttgcgggc gttaggtacg 300

cgtagttata aggtagttag taggttgtaa attggtttac ggttagcgtt ggggttaggg 360

tcgttttgtt ttcgggtagg cgaggtcgga gcggcggtaa gatggaaagg cggttattta 420

gagagttcga gtggagtcgg gattcgcgcg tcggtcgtgg gggttttagg gtagcgcgac 480

gcgttattac gaagatgtcg tcgtaggcgt cgagtagtag gagggcgggt agcgcgaagg 540

ttagtagggt ttagagcggt cggaagggtt cgaggttttt agttaggatc gagtagcgag 600

taggagtagg gggcggtgcg ggcggcgtgt cgagtaggga gagcgcgttt agtagtttcg 660

tcgcggttta tacggcggtg agtacgagta taggcggcgg tcgcgagttt ggtcgtagcg 720

ggtgtacgat gaggcggtag cgtgttaggt taagtgcggt tatttcgagc gtgtaggtcg 780

gtagtagagc ggcggagagg aagcgagcgg cgcggtatgg cgcggggttt aggcgtacgc 840

ggtttagttc gggcggcggt gcggttagta ggtttagcgg tatgatggag gcggtcgtta 900

gtaggtttac gacgtatagg tgcgttaggt agagcgcgtc gcgtagtttc ggcgtgcgta 960

gtattacgat tagtagcgcg tcgttgttta gtagtgtttt tatttttacg atagttgtta 1020

ggattaattt taacgagttt gcgatttttg aggcgtttag ttttgtggag ttggttattt 1080

gggtttttag gttttatttt 1100

<210> SEQ ID NO 23
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

ggtgtcggtg ttggtgttgt ttatggtcgc gttgtattag gtgtttaata agtggatatt 60

gggttaggta atttgcgatt tgtttatcgt tttcgacgtg ttgtgttgta ttttatttat 120

tttgtatttg tgcgttatcg cgttggatag gtattgggtt attacggatt ttatcgatta 180

cgtgaataag aggacgtttc ggcgcgtcgt tgcgtttatt tcgtttattt ggtttattgg 240

tttttttatt tttatttcgt ttatgttggg ttggcgtatt tcggaagatc gttcggattt 300

cgacgtatgt attattagta aggattatgg ttatattatt tattttattt ttggagtttt 360

ttatatttcg ttgttgttta tgttggtttt ttatgggcgt atatttcgag ttgcgcgttt 420

tcgtattcgt aagacggtta aaaaggtgga gaagatcgga gcggatattc gttatggagt 480

atttttcgtt tcgtagttta agaagagtgt gaatggagag tcggggagta ggaattggag 540

gttgggcgtg gagagtaagg ttgggggtgt tttgtgcgtt aatggcgcgg tgaggtaagg 600

<210> SEQ ID NO 24

<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

ttttgtttta tcgcgttatt ggcgtataga gtatttttag ttttgttttt tacgtttagt 60

ttttagtttt tgtttttcga tttttatttt atattttttt tgggttgcgg ggcgggagat 120

gttttatggc gggtgttcgt ttcggttttt tttattttttt tgatcgtttt gcggatgcgg 180

aagcgcgtag ttcggaatat gcgtttatag agaattagta tgagtagtag cgggatgtag 240

aaagttttaa aggtggaata gatagtgtag ttatgatttt tgttaatggt gtatgcgtcg 300

gggttcgagc ggtttttcgg ggtgcgttag tttagtatgg gcgggataga gatgaggaag 360

ttaataagtt aagtgagcga gatgagcgta gcggcgcgtc ggggcgtttt tttgtttacg 420

tagtcgatgg ggttcgtgat ggtttagtat ttgtttagcg cgatggcgta taggtgtaag 480

atggatgagg tgtagtatag tacgtcgagg gcgatgaata ggtcgtaggt tatttggttt 540

agtgtttatt tgttgagtat ttgatatagc gcggttatgg gtagtattaa tatcgatatt 600

<210> SEQ ID NO 25
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

gggatgataa gggagaaaaa tttttttacg gtttcgtttg gttcgcggcg tttgtttgtt 60

tgcgcggggt taaagttcgg cgtcgtttac gcgcggttcg ggtgggaatt cgtagacgtg 120

gggcgagtag ggtcgttggt tgtggcgggc gagcgtcggg gcgttacgtt cgaggtcgcg 180

gggtcggggt tgtaggtata gttcgagcgt ttttcgcggg gtttggtttt tgtcgttttt 240

cgtttcgtcg aatcggtatc gtcgtcgtcg gagtcgtagc gagtttttag agtttggttg 300

ttggcggtcg ggagcgtcgg gacggggcgc gaagtcggag gtttcgggac gtggatatag 360

gtaaaggtcg gcgggtcgga gtcgggcggg gcgcggcggc ggcgtttttc ggagggattt 420

ggtttcggtc gggttttatt tagtcgcggt ggttcgggtt tttacgttgg tttaggcggg 480

gacgtgttaa ggggttgggt tagggttgtc gttggtttgg tcgtttttcg ttcggcgggt 540

tttaggtgac gcggtcgcgg tttaattttc gtatttgagg ttttcggagc ggtttcgggg 600

cgcgtttatt tggaggttgg aattatatag ggtcgaaaaa gttgagtttt ggaggcgagg 660

cgttgtaggt gtggcggagg aggtcgggga aggtggggtg ggtgttaggg gtttagtatt 720

gaattttttt taggtttgag gtggggaatt gcgttttgtt taatttcgga gtttgtgggg 780

attatatagt ttttttacg gtcgattttt tttgtacggt tttatttttt tttgtttagt 840

ttattttagt 850

<210> SEQ ID NO 26
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

attgaaatgg gttagataaa ggaaagtgga atcgtgtaga gggaatcggt cgtggaaggg 60

gttgtgtggt ttttataagt ttcgaaatta aataagacgt agttttttat tttagatttg 120

gagagggttt agtattggat ttttggtatt tattttattt ttttcggttt ttttcgttat 180

atttatagcg tttcgttttt aggatttagt tttttcgatt ttgtgtaatt ttaattttta 240

-continued

ggtgggcgcg tttcgaggtc gtttcgagag ttttaggtgc gaaagttaag tcgcggtcgc 300

gttatttgag gttcgtcggg cgagaggcgg ttaggttagc ggtaatttta gtttagtttt 360

ttggtacgtt ttcgtttggg ttaacgtggg ggttcgggtt atcgcggttg ggtagggttc 420

ggtcgaggtt aggtttttc gagaggcgtc gtcgtcgcgt ttcgttcgat ttcgattcgt 480

cggtttttat ttgtatttac gtttcggagt tttcggtttc gcgtttcgtt tcggcgtttt 540

cggtcgttag tagttaggtt ttgaggattc gttgcggttt cggcggcggc gatgtcggtt 600

cggcgagacg ggaagcgata ggagttaaat ttcgcggaaa gcgttcgagt tgtgtttgta 660

gtttcgattt cgcggtttcg gacgtggcgt ttcggcgttc gttcgttata gttagcggtt 720

ttgttcgttt tacgtttgcg ggtttttatt cgagtcgcgc gtgggcggcg tcgggttttg 780

atttcgcgta ggtagataag cgtcgcgggt tagacggaat cgtgggaaag ttttttttt 840

ttgttatttt 850

<210> SEQ ID NO 27
<211> LENGTH: 1350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

tgaggtgtgg ggattattta tttcggtggg tttttttatt tttaggtcgg tttttttatt 60

acgcgtgggt gtgggggtat tgttttcgtt gcgcgtagga atagcgggga gagttaggag 120

cggagcggtt tcgggatgtt agattgagta gtgggttcgt ttgcggttat tttttaggga 180

ataagttttt tttcgcggag attttgtttt ttttaaaagt ttttttgggt ttagtttagg 240

gcgataggac gattttttt gggaagggag agtttgttag ttttttttt attcgttagg 300

cggtgtagtt tttttttcg ttcggggcgc gcgtatttta gcgtcgcggg tttagcgttt 360

agtagtcgcg ttttaggtcg ggtttcgggt ttcgggagtt cgtaggcgcg cgttcggtcg 420

ggcgtgtcgg gagcgcgcgg cggtcggggg cggagcgtag ttagggttgc gcggcgcgtt 480

tcggttttcg ttcgttttta gtcgggtttt ttagcggtcg gcgggacggt tttcggttgt 540

agtttgttcg ttcgtttcgc gcgggggtcg agtcgcgaag cgcgtttgcg attcggcgtt 600

cgggcgcgtt ggagaggacg cgaggagtta tgaggcgtta gtttgcgaag gtggcggcgt 660

tgttgttcgg gttgttttg gaggtagggg tcggggatcg ggtgttgtcg gaggcgcggc 720

gtttattatg ttggcggttg ggggcgcgta gtttcgaggc gttttagagg attttgtttg 780

ggagcgtaga cggtggagcg acggggagtt atagttttgc gcgtttttcg gagttgggag 840

gtgcgggatt ttggtgacgg ggaggttttc gtttcggttc gcgtttttcg tcgtttttc 900

ggttttcgta tttcgttttt atttgcgggg tgagcgcgtt tttcgcgtcg atcgttttcg 960

ttagttcggg gtgattttg tgtatcgttc gttttttttt ttcgtcgtag agggtcgagg 1020

atcggatgga ttcggggttg ggcgggggtg gttttcgggc gcggcgtagg cgcggagagt 1080

tcggggcgtc gggtagtttg gggttaggaa aggatgggtg tcgagtcggg gtgaggggag 1140

cgggcggagg ggattgtggg gaagtgtcgc gggagtgtcg ggagttgtgg aggtgagtag 1200

cgggaggagg cgttttcgcg tgtgaaaatg aagtgtagtt tttaggtgcg gggaggaaat 1260

tttgcggaga gtttggttgg gtgggggtgc ggagtcgaag tcggcgggga atttgttgag 1320

cggttttcgg gtgcgagcgt tcgtgatcgt 1350

<210> SEQ ID NO 28
<211> LENGTH: 1350
<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

gcggttacgg gcgttcgtat tcggaagtcg tttaataagt ttttcgtcgg tttcggtttc 60

gtatttttat ttagttaggt ttttcgtaga attttttttt cgtatttaaa ggttgtattt 120

tatttttata cgcgggaacg tttttttttcg ttgtttattt ttataatttt cggtattttc 180

gcgatatttt tttatagttt ttttcgttcg tttttttat ttcggttcgg tatttatttt 240

tttttaattt taaattgttc ggcgtttcgg gtttttcgcg tttgcgtcgc gttcgaggat 300

tattttcgtt taatttcggg tttattcgat tttcggtttt ttgcggcggg gagaggggggc 360

ggacggtgta taaaggttat ttcgagttaa cggaggcggt cggcgcggga aacgcgttta 420

ttcgtagggt gggggcgggg tgcgaaaatc gaaggaacga cggaaggcgc ggatcggggc 480

gggagttttt tcgttattag ggtttcgtat tttttagttt cgggaggcgc gtagggttgt 540

ggtttttcgt cgttttatcg tttgcgtttt taggtaaggt tttttggggc gtttcggaat 600

tgcgcgtttt tagtcgttag tatggtgggc gtcgcgtttt cggtagtatt cggttttcgg 660

tttttatttt taagagtagt tcgagtagta gcgtcgttat tttcgtaggt tggcgtttta 720

tggtttttcg cgtttttttt agcgcgttcg gacgtcgggt cgtaggcgcg tttcgcgatt 780

cggttttcgc gcggggcggg cgggtagatt gtagtcggga gtcgtttcgt cgatcgttgg 840

ggggttcggt tgggagcggg cgggagtcgg ggcgcgtcgc gtagttttgg ttgcgtttcg 900

ttttcggtcg tcgcgcgttt tcgatacgtt cggtcgggcg cgcgtttgcg ggttttcgga 960

attcgaggtt cggtttgggg cgcggttgtt gggcgttagg ttcgcgacgt tgaggtgcgc 1020

gcgtttcggg cgggaggagg ggttgtatcg tttggcgaat gggaggggga ttggtaggtt 1080

tttttttttt aagggaggtc gttttgtcgt tttagattaa atttaggaag gtttttaaaa 1140

gaagtagagt tttcgcgggg ggaagtttgt tttttgagag gtggtcgtag acgaatttat 1200

tgtttagttt ggtatttcga agtcgtttcg tttttggttt ttttcgttgt ttttgcgcgt 1260

agcgggggta gtgtttttat atttacgcgt gatgggaagg tcggtttggg ggtgggaagg 1320

tttatcgaaa tagatggttt ttatatttta 1350

<210> SEQ ID NO 29
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

aatttagaaa taaataaata tatatgtata cgtatataaa tatattttaa attaaaaaat 60

atttttagat agtggtatgt attatattta gaaattaata acgaagtaaa ttatgggatg 120

ttatttacgt ttgttttaaa ggtatcgaat ttataaatta ttttaggtgc ggagtaggat 180

aggttgaaaa taggaatgat atgaattcgc gcggaatagt tgtcggcgcg gtgtttaggg 240

cggtatttcg ttcggtttcg gtttttttag ttttgggttc gatttttatt acgtttttgt 300

ttcgacgcga acgcggagtt cgagcgcgcg ttacgtcgtg tggggtcgaa gaggttgtta 360

tttagaggcg gagtgcgggt tcgcgagggt ttttattcga ttttcgtttt cgttagtatt 420

tacggattcg cgttttcgtc gcgcgtcgat tcgggagtag tatcgttttc ggtataggag 480

ttttacgcgt tttttattta ataggaagtt gggtggaagt agcgcggatt tacggtatat 540

cgaacgtatt ttaatagaat tcgacgtaga tacgcgtttt taatcggcgg agatattggt 600

agggttagaa acgcgcgtag cgggggcggg aggtcggtaa gtttttcgtt tttgttcgag 660

-continued

atttcgtttc ggttcggttt cgtttttttt tttgtttttt tttttgtac gtacgggttt 720

cgtttttcgc gcgacgtttt ttgttgattc ggaaacggat ttttcggagt cgaggttcgt 780

tcgggtgagt gtttttcgtt ttttgtggtt aaatttagtt acgtagtttt tttttgcgg 840

cgtttttat attcggggtt tgttggtttt cgcggatgtt ataggttcgg taatcgtttt 900

tttgtcggcg gggagtttcg cgacgttcgg aaatgtttcg aagtttgtcg tttagttgtt 960

agatttgcgt ttgtgttcgg tttcgttatt gaggtcgttt ttgttcggtt tttttatttt 1020

agtttttttt atcgttcgtt tattttatcg cgcgcggttt taggtttcga ttcggtatgt 1080

ggtttgtttt ttatcgtttt 1100

<210> SEQ ID NO 30
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 30

gggacgatgg aagataagtt atatgtcgaa tcgggatttg aggtcgcgcg cgataggatg 60

ggcggacggt gaagagaatt agggtggaag ggtcggatag gggcgatttt agtgacggaa 120

tcggatatag acgtagattt ggtagttggg cgataggttt cggagtattt tcgggcgtcg 180

cgggattttt cgtcgatagg agggcggttg tcgagtttgt gatattcgcg gagattagta 240

gatttcgggt gtggaggacg tcgtaggaag ggaattgcgt ggttgggttt ggttataaaa 300

agcggagggt atttattcga gcggatttcg gtttcggaga attcgttttc gggttaataa 360

aaaacgtcgc gcgaggggcg gggttcgtac gtgtagggag gggaggtaga gaaaaaggcg 420

gggtcgggtc ggggcggggt ttcgggtagg ggcggggagt ttatcgattt ttcgttttcg 480

ttgcgcgcgt ttttggtttt gttagtgttt tcgtcggttg aaagcgcgtg tttgcgtcgg 540

gttttgttgg agtgcgttcg gtgtgtcgtg ggttcgcgtt gtttttattt aatttttttgt 600

taggtaagag gcgcgtgagg tttttgtgtc gggggcggtg ttgttttcga gtcggcgcgc 660

ggcggggacg cgagttcgta ggtgttggcg ggagcgagag tcgggtgggg attttcgcga 720

gttcgtattt cgtttttggg tagtagtttt ttcggtttta tacggcgtga cgcgcgttcg 780

ggtttcgcgt tcgcgtcgag gtagaggcgt agtaggggtc gggtttaggg ttggaggggt 840

cgggatcggg cggggtgtcg ttttggatat cgcgtcggta gttgtttcgc gcgggtttat 900

gttattttta tttttaattt gttttgtttc gtatttgaga tgatttataa attcggtatt 960

tttgggatag gcgtggatga tattttataa tttatttcgt tattaatttt taaatgtaat 1020

atatattatt atttaaaagt atttttttaat ttgaaatata tttgtatacg tatatatgta 1080

tatttattta tttttgaatt 1100

<210> SEQ ID NO 31
<211> LENGTH: 1350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 31

tgcgcgttgt tgcgttgagg tcgaatgaag cgtagtacgg tgcgggtagt tcgaggtttc 60

gaggttgggt tttgtttgtt tgggattgcg tcgtgtttag tttcggtttt ttttttgtgg 120

gtaaggatgg ttgagtttag tttttacggt agcggttttt tgtgttatta gtagtttttt 180

ttttgcgttt ttcgtttttt tttttagat tggattttttt ttttttttcg cgtttttttt 240

ttcgtatttt ttattcgttg gttttttttt tagttgtttt tttttaggt ttttttggt 300 tgcgcgcgtt ttttttttcg tttttttttt tttcgtagtt tcgtcgtttt ggtgtttttt 360

tgttcggttc ggtcggcgtt cgttttcggt ttcggtttcg ttagttcggg ttttcgcgtt 420

cggagtagtt tagttttgta gtggttcggg attcgatgtt atgagaggga agcgagtcgg 480

gcgtttagat ttttaggagg cgtcggatgc gcggcgggtt ttgggatcgg gttttttttt 540

cggttcgttt tgttttcggg tgattatttg gtttcgttta tagttttgtt tttttcggag 600

gagttatcgg tgtcgcgtgc gtgtggagta tttgtagata tgattgcgtg gaggagattt 660

tagtcgttgt ttttgttttt cgggttgttg gtgttgtgcg cgaggttttt tattgtagcg 720

aagggtaaga cggatttgtt tttggtcggg gaggcggtag agttttcgga ggtttcgtgt 780

gcggacgcga gtgtgcgttt tggggatcgt agggtacgga gtggtcgttt ttgttcggcg 840

ttgttttatc gtcgaagttc ggggaacgcg atgtacggga gggagttttt atcgcgtttt 900

ttttagtttt tttgggtttt cgttttattt cgttattttt tttttttttt ttgggtttat 960

aggagagatt tttttttttc ggtagtatag ggtgttaagg agaaaggaat ttaatacgag 1020

ttgggttgga attgtgtttc gtcggggcgg tgttgttttt ttcgagacgt ggattttacg 1080

ggtcggggtg gttgaggggt agtttttagg attttttttt cggattcgac gcgtttggga 1140

aagcgtttcg ggtgaagtcg gtttggaaag ttcgggtttt ttacgggggt tttggtatta 1200

ataggtaaag gttttcgtcg gttcggtttt ttcgtattta tatattttat tttttttttt 1260

tttttttttt ttttaacgtt tttagtcggc gaggagtagt tgtttttaga aggtcgtttt 1320

cgtttttttt tttttcggat ttcgtttttt 1350

<210> SEQ ID NO 32
<211> LENGTH: 1350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 32

aaggagcgaa gttcggggga gaggaaagcg ggggcgattt tttagaggta gttatttttc 60

gtcggttgag gacgttggag agggaaggag gagaggagga atggggtgta tgggtgcgag 120

gaggtcgggt cggcggagat ttttgtttat tggtattaaa attttcgtag agagttcgaa 180

ttttttaggt cggttttatt cgggacgttt ttttaggcgc gtcgggttcg gggagaaagt 240

tttgggaatt gtttttttagt tatttcgatt cgtggagttt acgtttcgga ggaggtaata 300

tcgtttcggc ggagtatagt tttagtttaa ttcgtattgg gttttttttt ttttgatatt 360

ttgtattgtc gagaaaaaga gatttttttt gtgagtttaa gagaggggga aggaatggcg 420

gggtggggcg ggggtttagg agggttgggg agagcgcgat ggaagttttt tttcgtgtat 480

cgcgtttttc gagtttcggc gatggagtag cgtcgggtag aggcggttat ttcgtatttt 540

gcggttttta aaacgtatat tcgcgttcgt atacggggtt ttcgagggtt ttatcgtttt 600

ttcggttagg agtaagttcg ttttattttt cgttgtagtg aggagtttcg cgtatagtat 660

tagtagttcg agaagtagga gtagcgattg gaattttttt tacgtagtta tgtttgtaga 720

tattttatac gtacgcgata tcgatggttt tttcgaggaa ggtagggtta tgagcggagt 780

taaataatta ttcgagggta aggcgagtcg gagagagagt tcggttttaa gattcgtcgc 840

gtattcgacg tttttttgaag gtttgggcgt tcggttcgtt ttttttttat agtatcgggt 900

ttcgagttat tgtagggttg agttgtttcg agcgcggaga ttcgggttgg cggggtcggg 960

gtcggggacg agcgtcggtc gagtcgggta ggaaggtatt aaggcggcga ggttgcggga 1020

gggggagaag cggggagagg agcgcgcgta gttaggagag atttggagag gaggtagttg 1080

-continued

gagagagagt tagcgagtgg gagatgcggg gaggggggcg cggggggggag gagagattta 1140

gtttagagag aaaaggcgga gagcgtagaa gaagggttgt tagtggtata aggagtcgtt 1200

gtcgtggagg ttggatttaa ttatttttat ttatagagag gggatcgagg ttgggtacgg 1260

cgtagtttta gatagataga gtttagtttc ggggtttcgg gttgttcgta tcgtgttgcg 1320

ttttattcgg ttttagcgta gtagcgcgta 1350

<210> SEQ ID NO 33
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 33

gatttttgg gttaggatat gtgagagttg cgtaggtttg ggttcggcgt ggcggaggtg 60

cgcgagagcg gttagaagag ggcgttagag agttaggcgc ggttcgcgga ggagttcgcg 120

tcggttttta tatttagttt cgcgtcgcgc ggatttatcg agttcgcgtt tagacgtttt 180

agttttatcg agaggtcgtt cgggtcgtgt tttttttttt ttttaggtgt aggtagagtt 240

ttcgagttat ggttagtttt ttcggtagtt tcgaagttat tggtaagttt cgaggtaggg 300

atggtcggtt taggagggag gaggacgacg ttttttttcga agagaagagg ttggggttgt 360

agttggaggg gggaagcgta tagttcgagg attgcgagaa cggggaggac gcgtcgcggt 420

taggtaggga ggagatcggt atttagatag gtggcgatcg tagaggagta agtgacgcgg 480

gcgttggggt tcgggggtgt cgggggcgtc ggtaggggcg gcgggaggtt tcgtggtcgg 540

tttcgggttg aagttggtat tttagcggta atttcgaagg gcgcggagtg atagcgcgtg 600

acggttttcg agacgttagt tgtcgttttt cggttgtgtg gttttgattt tttgattttt 660

ttacgacgtc gttggttggg agatttattg gattttgcgg ttggttaaaa agagaggggt 720

agtttcgcgt tttgggggtt tttagtaggg gaagtggcgg gtgttgcgtt gggtattttg 780

tttggggtat ttgtttggga ttttgttggt gtttttttatt tggcgagggg ttagtggtgg 840

gggtaggggg 850

<210> SEQ ID NO 34
<211> LENGTH: 850
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 34

ttttttattt ttattattgg tttttcgtta ggtgagaggt attaataggg ttttagatag 60

atgttttaga taggatgttt agcgtaatat tcgttatttt ttttgttagg ggtttttagg 120

acgcggggtt gttttttttt ttttggttag tcgtagagtt tagtgggttt tttagttagc 180

gacgtcgtgg gagaattagg aagttaaagt tatatagtcg agaagcggta gttggcgttt 240

cggaggtcgt tacgcgttgt tatttcgcgt ttttcggagt tgtcgttaaa atattaattt 300

taattcgggg tcggttacgg agtttttcgt cgtttttatc ggcgttttcg gtattttcgg 360

attttagcgt tcgcgttatt tatttttttg cggtcgttat ttgtttgggt gtcggttttt 420

tttttgtttg gtcgcggcgc gtttttttcg ttttcgtagt tttcgggttg tgcgtttttt 480

ttttttagtt atagttttag tttttttttt tcgggaggga cgtcgttttt tttttttttg 540

ggtcggttat ttttgtttcg gggtttgtta gtggtttcgg agttgtcgga agggttggtt 600

atggttcggg ggttttgttt gtatttggag aagaggaagg atacggttcg agcggttttt 660

cggtggagtt ggggcgtttg agcgcgggtt cggtgggttc gcgcggcgcg gagttgggta 720

-continued

tagggtcgg cgcgggtttt ttcgcgggtc gcgtttggtt ttttggcgtt tttttttggt 780

cgttttcgcg tattttcgtt acgtcgggtt taggtttgcg tagtttttat atgttttggt 840

ttaggaggtt 850

<210> SEQ ID NO 35
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 35

tcggcgttta ggtgacgttg attttgttgg tttatcgttt tgggggttat ttaattttt 60

agcgatgttt tttagttggg gaggttaaga agtgtttcgt ttaaggtttt ttaatattcg 120

atttttagat ttttaatttt gggttagtta tatcgtaaat ttttttagtt gtttttttg 180

cgttttgcgt tttttttta cgttatttgt tagggagtcg ttaaatagta agatcgcgcg 240

ttttgcggtt ttagagtgcg gatttcggtc gcgtgcggtt ttgatcgcgt cgttttattt 300

ttggcggggt tacgtacgga cgttatggtt ggcgtcgcgg agtcgggcga tgcgcgcgga 360

ttttttcggg gttttgattg tttttgagtt ttttttgcgg ggggcgtgcg cggttcgttt 420

ttcgcggcgt tacgcggttt tttttcggtc ggggattggt gcgtcgggcg gggcggggcg 480

gggcgggata aaggcgcggg gtttggttgc gcggggtttg cgggtagttt taattttggg 540

ttcgtagttt gcgttgggtg cgtaggaagg ttagtgtggg ggtcgttcga tatttttttt 600

tcgcggaggt gggagtcgag ttatattttg gagtggggat tggtcgcgga gcgggttgtt 660

tagggtcggt cgaggtcggg gcgagttttg cgcggcgttg gagattttgt attttcgggc 720

gcgcgtaggg ttttcggtcg tggtcgtaga gttaggaggg gcggtttcgg agttcggcgc 780

ggggagggtt taggcgtagt cggggttggt agggcgcgat attcgttttt ttttattttt 840

gaaagggttt tttacgtcga gaagaggggc gggtatggtc ggttcggcga aatcggtttg 900

tatagatttt gggaagttat cgtttgcgga gggtgggatt ttatagtttg tttatttgtt 960

taggttgaga tttcgtgttt tagttttgga tgttttacgg gtttttcgtt tcgggtagcg 1020

gcgtacggga ggagaagatt ttcggtttgt agttagattt ttttttgaga ttttttttag 1080

tttaggttta gagttttggg 1100

<210> SEQ ID NO 36
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 36

tttaaagttt taagtttgag ttagggaggg ttttagaggg aggtttgatt gtagatcggg 60

agtttttttt tttcgtgcgt cgttgttcgg gacgagaaat tcgtggggta tttaggatta 120

ggatacgagg ttttagtttg ggtaggtgga taagttgtgg ggttttattt ttcgtaggcg 180

atggtttttt aaagtttgta taaatcggtt tcgtcgggtc ggttatgttc gttttttttt 240

tcggcgtggg aagttttttt aaaagtggag gggagcgagt gtcgcgtttt gttaatttcg 300

attgcgtttg ggttttttttc gcgtcgggtt tcggagtcgt tttttttgat tttgcgatta 360

cggtcgggga ttttgcgcgc gttcgggaat gtagagtttt tagcgtcgcg tagggttcgt 420

ttcgatttcg gtcggttttg ggtaattcgt ttcgcggtta gtttttattt taagatgtgg 480

ttcggttttt attttcgcgg gggggaaatg tcgggcgatt tttatattga tttttttgcg 540

tatttagcgt aaattacgaa tttagagttg gagttgttcg tagatttcgc gtagttagat 600

-continued

ttcgcgtttt tatttcgttt cgtttcgttt cgttcggcgt attaattttc ggtcgaggag 660

gggtcgcgtg gcgtcgcggg gggcgggtcg cgtacgtttt tcgtagggag gatttaggga 720

tagttagggt ttcgggagag ttcgcgcgta tcgttcggtt tcgcggcgtt agttatggcg 780

ttcgtgcgtg gtttcgttag ggatggggcg acgcggttag agtcgtacgc gatcgaaatt 840

cgtattttgg agtcgtagag cgcgcggttt tgttgtttag cggtttttttg gtaagtgacg 900

tggggaagaa acgtagggcg taggagagat agttggaaag gtttgcggtg tagttggttt 960

aggattgagg gtttggaggt cgggtgttgg aagattttga gcgaggtatt ttttggtttt 1020

tttagttggg aggtatcgtt gaaaaattag gtgattttta agacggtaga ttagtagagt 1080

tagcgttatt tgggcgtcgg 1100

<210> SEQ ID NO 37
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 37

aaagttaagc gtcgtcgtta tttaaggtat tgcgttgatg cgttgcgggt cgattaggtg 60

ttttcgtcgg ggcgtttttt tttacgtagg aagggttacg tcgagagagg taggtaataa 120

gggtacggtt ggaggtcgga aggttatttc gttttcggcg gggcgggcgc ggtttagttt 180

tatttttcgg gtacgttcgg gcggggcgat tgtagggaac ggggcgggga ggcgatagtt 240

ttcggtttcg tcgcgcgtta gttcgttttc gttgttcgga ggcgtcgtag gtttgggttt 300

tcggatagtt gagttcgagc gtcgtttttc gaaaggtgaa ggcggttcgg ggaggcgggg 360

acggtgacgg gggcgggggt cgcgggcggt ttttcgacgg ttgtcgcggg gttagtttaa 420

agttttcgat tttcggtagt tgcgtttttc gcgcggggcg tcggagtagg gcgggttaag 480

ttggtttgcg gtcgcggcgg gaagaagggt tagcgaagta ttttcgatcg ggtttaggcg 540

tcggacgtcg gggggcgttt cgttgtaatt tttttttgga agtttcgata cgagtttcgg 600

ttcgcgcgcg cgttttttta cggttacgcg cgtattttgt cgttcgtatt ttcgcgcgtt 660

tttcgtttat tttttttttt tttttttatt tttatatttt aaaataggtt aaggggtgga 720

agttatattt ggtgtagttt tcggttttga tgtaaaagta gtttttgttt ttggttgcgg 780

gatagcgttg tgattattcg taacgggaga gttgttgtta gtcgttatat cgtgcggaaa 840

gcgtcggcga tcggagtatt gataatggtt tgtatagggg agcggagaga agtttttgtt 900

gcgttttaga ttcgttgttt cggcgttcgt tcgtagggag gagggggcgc gataggtcgt 960

ttagcgcgtg tttcggagtt cgcgttcggg tttggtcgtt tgggtgagtt tttgttcgtt 1020

ttttgttttt ttagtagttc ggggtggttg tttattttgt aaatagtttt gtaatacgat 1080

taaaataggc gagatagtta 1100

<210> SEQ ID NO 38
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 38

tggttgtttc gtttgttttg atcgtattgt aaggttgttt gtaaggtaaa tagttatttc 60

gggttattgg aaaggtaggg gacgagtagg aatttattta ggcggttaga ttcgggcgcg 120

ggtttcgggg tacgcgttag acgatttgtc gcgttttttt tttttgcgg gcgggcgtcg 180

aggtagcgga tttagggcgt aatagaagtt ttttttcgtt tttttatgta gattattgtt 240

```
agtgtttcgg tcgtcggcgt ttttcgtacg gtgtggcgat tggtagtagt tttttcgttg    300

cgagtagtta tagcgttgtt tcgtagttag gggtaaaagt tgtttttgta ttagagtcga    360

gggttgtatt aggtgtaatt tttattttt gatttatttt agagtgtgag gatgaaagga    420

agaggaaaaa atagacggag ggcgcgcggg ggtgcgggcg gtagggtgcg cgcgtggtcg    480

tgggggagcg cgcgcgcggg tcggggttcg tgtcggggtt tttaaagaga agttgtagcg    540

aggcgttttt cggcgttcgg cgtttgggtt cggtcggggg tgtttcgtta gttttttttt    600

tcgtcgcggt cgtaggttag tttggttcgt tttatttcgg cgtttcgcgc gggaagcgta    660

gttatcgggg atcgggggtt ttgggttggt ttcgcgatag tcgtcgggag atcgttcgcg    720

gttttcgttt tcgttatcgt tttcgttttt tcgggtcgtt tttatttttc gggaggcggc    780

gttcgggttt agttgttcgg gaatttaggt ttgcggcgtt ttcgggtagc gaaggcgggt    840

tggcgcgcgg cggagtcggg gattgtcgtt ttttcgtttc gtttttgta atcgtttcgt    900

tcgaacgtgt tcgggaagtg aggttgggtc gcgttcgttt cgtcggggac ggggtgattt    960

ttcggttttt agtcgtgttt ttgttgtttg tttttttcgg cgtggttttt tttgcgtagg   1020

agaagacgtt tcggcgggag tatttggtcg gttcgtagcg tattagcgta gtattttggg   1080

tgacgacgac gtttggtttt                                               1100


<210> SEQ ID NO 39
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 39

gcgattttag aggagtaatc gggttttaat tttttgcgtt cgttttgtta taattttttt     60

ttatttattt ttattttatt tttataatat tttttattgg gggggttttt tgtgtttcgg    120

attttttttt ttatggtttt tttagtcgaa gtcgggggtt ttttgggcgg tttggagggt    180

ttgggttagt aggtgggttc gtattttttg ttgtttttttg tcggggagcg gtcgtcgttg    240

ttgggcgagc gtaggagcgc ggcggagcgg agcgcgcgcg gcgggtcggg ggttgcgtag    300

ttggcgtatt tgtacggtat tttgcgtcgt cggtagtttt attgtcgtat cggtttttat    360

ttgtagattt tgttcgacgg tagcgtgtag ggtattcggt aggattatag tttttttcggt    420

acgtattagt atttcgattt tatttttatt tgcgttttag ttcggttttt cgtttttttt    480

ttttgtattt tttttttgt ttgttaaggg cgttatcgtc gcgcggagtt cggagttttt    540

ttggatttat tcggtgtaag acgtaggttg ggttgaagg gttggttaga gtagtcgcgg    600


<210> SEQ ID NO 40
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

tcgcggttgt tttggttagt tttttagttt tagtttgcgt tttgtatcgg atgggtttag     60

gggagtttcg ggtttcgcgc ggcgatgacg tttttggtag gtaaagaggg aggtgtaagg    120

ggagggaacg aggagtcgag ttggggcgta gatgggggtg gggtcgggat gttagtacgt    180

atcgaagagg ttgtggtttt gtcgggtgtt ttgtacgttg tcgtcgggta ggatttgtag    240

gtggaagtcg gtgcggtaat agagttgtcg gcggcgtagg atgtcgtgta ggtgcgttag    300

ttgcgtagtt ttcggttcgt cgcgcgcgtt tcgtttcgtc gcgtttttgc gttcgtttag    360

tagcggcggt cgtttttcgg taggaggtaa taggaaatgc gaatttattt gttggtttaa    420
```

-continued

gtttttagg tcgtttagaa agttttcgat ttcggttaag ggagttatgg agggggagat 480

tcggaatata aaagattttt ttagtaaaga gtgttgtggg ggtgggatgg aggtggatag 540

agaaaaatta tagtaaaacg agcgtaaaaa gttaaggttc ggttattttt ttgaggtcgt 600

<210> SEQ ID NO 41
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

tatattttat ttgtgtcgta tatgtgaaga tataattgta aatcgtttac gattttgagt 60

taagattttg agtttttga ggttaggaga tcgttaggga atgtgagtgt tttagacggg 120

cgttgagttt agttcggaga tttatttcgt tcgtagtagc ggcgcgggtt ttagagagtt 180

tcgtattcgg tcgcgtttta gttacgttga ttcggttgtg ttcgtagtgt cgcgttgtcg 240

cgtagttagg tgtcgtcggg ttggcgcggt tatttatgat tgcgtggttg ggttgggggt 300

tcggggtcgg ggagtagtcg ggattcgtcg ttttttttat gatttttcg ggtcgaatta 360

cgggatcgtt acgttgaagg tggcgtcgcg ggttttcggg gtcgcgcgag tgtaggggtc 420

gttttcggtc ggtcgcgaag ttcgcggtat cgatttttcg cgagatttcg gcgatttttt 480

ttttcgtttt cgttttttcg tttttgttt tttttagtt ttggtgtggg cggttttcgt 540

tatggttgcg ttgcgaaggt ttttgtggtc gttatttcgg gtgttttttt tattttgcgt 600

ttattagttt tttttgggt cgtgggggcg gtttgcggtg attattttgg gtttttttgg 660

tcggtttttt ttttttcgag aggatgagga gagggttgtg gcggaggcgg tatggaggcg 720

gcggcggcgt tgggggagt tgagcgtggc ggcggcggtc ggcgggggt tggtcggttt 780

ggtatgttat tagttgtacg gggattttag ggtcggttcg tcggcgatcg ggcgattttt 840

aaagagcgcg gttacggagt tcgaggattc gtttcgcggt cgggggatgt tgtttatttt 900

agtggcggtt gttaaggaga cggtgagtgc gcgagcgcgc gttatatttg cgcgggggat 960

gtgattttcg tgtcgggtac gtaggatttt ggaggttgtg gggacggtgt aagcgttgtg 1020

gtcgcgggtg aggaattttt cgtgagcgag gttgatattt aggtcggata gtttaggatt 1080

cggttattta cgtattggga 1100

<210> SEQ ID NO 42
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 42

ttttaatacg tgggtgatcg gattttaggt tgttcggttt aggtgttagt ttcgtttacg 60

ggaagttttt tattcgcggt tatagcgttt gtatcgtttt tatagttttt agggttttgc 120

gtattcggta cgaaggttat atttttcgcg taggtgtgac gcgcgttcgc gtatttatcg 180

tttttttggt agtcgttatt gggatgggta gtatttttcg gtcgcggggc gggttttcgg 240

gtttcgtggt cgcgtttttt gagggtcgtt cggtcgtcgg cgagtcggtt ttggggtttt 300

cgtatagttg gtagtatatt aggtcgatta gtttttcgtc ggtcgtcgtc gttacgttta 360

gtttttttta gcgtcgtcgt cgtttttatg tcgttttcgt tatagttttt tttttatttt 420

ttcgggagga gaagggtcgg ttaggaaggt ttagggtggt tatcgtaggt cgtttttacg 480

gtttaaggag gggttggtga gcgtagagtg gaggagatat tcggggtggc ggttataaga 540

gttttcgtag cgtagttata gcggaggtcg tttatattag agttgggagg gggtagagaa 600

-continued

cggaggggcg ggggcggggg ggggggtcgt cgaaatttcg cgagaagtcg gtgtcgcgag 660

tttcgcggtc ggtcgagagc gatttttata ttcgcgcggt ttcggggatt cgcgacgtta 720

tttttagcgt agcggtttcg tggttcggtt cgggaagatt atggaagagg cggcggattt 780

cggttgtttt tcggtttcga atttttagtt taattacgta gttataaata atcgcgttag 840

ttcggcgata tttggttacg cgatagcgcg atattgcggg tatagtcgag ttagcgtaat 900

tgaggcgcgg tcgagtgcgg ggtttttttgg ggttcgcgtc gttgttacgg gcggggtggg 960

ttttcgagtt gggtttagcg ttcgtttggg atatttatat tttttaacgg ttttttgatt 1020

ttaggaaatt taaggttttg atttaaggtc gtgaacgatt tgtaattgta tttttatata 1080

tacgatataa atgaggtata 1100

<210> SEQ ID NO 43
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 43

gtttgggtac gcgggatagg ttgtattcgt ttgttagagg cgttttatcg aggcgttacg 60

ggtgaagttt tcggttttat ttacggggcg gggtttcggt tcggttcgat tattgttcgc 120

ggtgggggag ggggatggat tacgttacgc gttaaaggcg atcgcgattt ttttttttgta 180

ggtagtttgg aaggtttttt tttttttttt acgttatttt tttcgtggta ttgaaaagtt 240

tcgttttttt tttttagttt cgtttttttc gagcgttttt tttattgttt ggaatggtgc 300

ggttttaggt cgcgggttac gcggcggagg gggcgtggtt tgttttcggt ttagtcggtt 360

tttttttgtt tttgttggag ttcggggagt ggcgttggtt gttagagcga tgtcgggtcg 420

gagttgcgtc gttttagttt ttttggttgt cgtcgttagt tgtgtcgtcg cgtagtacgc 480

gtcgtcggtg agtgagtttg agtcgaggcg tagagagggg cgtgtaggtg cgggcgcgga 540

tggaggcgta ggtgtggcgg cgcgagcggg tataaggaat atttcgtgtt gggtagtttt 600

<210> SEQ ID NO 44
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

gaagttgttt agtacgaggt gtttttttgta ttcgttcgcg tcgttatatt tgcgttttta 60

ttcgcgttcg tatttgtacg tttttttttg cgtttcggtt taagtttatt tatcggcggc 120

gcgtgttgcg cgacggtata gttgacggcg gtagttagga ggattaaggc gacgtaattt 180

cggttcggta tcgttttagt agttaacgtt atttttcgga ttttagtaga ggtaaagaag 240

agtcggttgg gtcgggggta ggttacgttt ttttcgtcgc gtgattcgcg atttgggatc 300

gtattatttt aggtagtagg gggaacgttc ggaggaggcg ggattgggag gagaggacgg 360

ggttttttag tgttacgaaa agggtggcgt agagaaagag agagagtttt ttaggttatt 420

tgtagaagga gagtcgcgat cgtttttggc gcgtggcgtg atttattttt tttttttatc 480

gcgggtaata gtcggatcga gtcggagttt cgtttcgtag gtggggtcgg gagttttatt 540

cgtggcgttt cgatggggcg tttttagtag gcgggtgtag tttgtttcgc gtatttaggt 600

<210> SEQ ID NO 45
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 45

ggtagtgtag ttgtgggaat ttttttacgc gtacgaattt agttaacgat ttttgataga 60

tttttgggag tttgattaga gatgtaaggg gtgaaggagc gttttttatc gttagggaat 120

tttggggata gagcgtttcg gtcgtttgat ggtcgaggta gggtgcgatt taggatttag 180

gacggcgtcg ggaattatat tatggttcgg atttttaaga ttttaaagtt cgtcgtcgtt 240

atcgtcgcgg ttttgttgtt agtgagtttc ggtcgcggtt tttggttggg gaagagcgta 300

tttggcgtcg ggagggggta gggagacggg gatacggtag ggatgtttgg ttttggttat 360

ttgcggtcgg gtatgttcgg gtaggacgaa ttcgtcgtcg gagttagggg aagaattggg 420

ttttcgggtt gggtaggagg gattcggtcg cgagggagta gagaggcggt ttttttggtt 480

gtttcgagtt cgcgaaggga gggaagtttt agaatcgaga gagggaggga gttaaggtgg 540

aatttataga gtgagttttt tgaagatata gagcggttgt tttttttatt aattaattaa 600

<210> SEQ ID NO 46
<211> LENGTH: 600
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 46

ttaattaatt aatgagagag gtaatcgttt tgtgttttta ggaggtttat tttatgggtt 60

ttattttgat tttttttttt tttcgatttt ggaatttttt ttttttcgcg ggttcggggt 120

agttaggggg atcgtttttt tgttttttcg cggtcgggtt tttttgttt agttcgggga 180

tttagttttt tttttgattt cgacggcgag ttcgttttgt tcggatatgt tcggtcgtag 240

gtgattaggg ttaggtattt ttgtcgtgtt ttcgtttttt tgttttttttt cggcgttagg 300

tgcgtttttt tttagttagg gatcgcggtc gggatttatt ggtagtagga tcgcgacgat 360

gacgacgacg aattttaggg ttttggggat tcgggttatg gtatggtttt cgacgtcgtt 420

ttgggttttg ggtcgtattt tgtttcggtt attaggcggt cggggcgttt tgtttttaga 480

gtttttttaac ggtaggaagc gttttttttat tttttgtatt tttggttaaa tttttaaaaa 540

tttattagaa atcgttggtt gagttcgtgc gcgtggagag gtttttatag ttgtattgtt 600

<210> SEQ ID NO 47
<211> LENGTH: 1100
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 47

cgtttgcgga ggattgcgtt gacgagattt ttatttattg ttattaattt gtggtggaat 60

ttgtagttgt atattggatt tgattcgttt cgtttcgaat gacgtttgtt cggaggtagt 120

gaaagtatag tcgcgtcgtt ttaagttagt ttggatatat aaattagtac gcggtcggag 180

aatttcgtaa tttttgcgtt tataaaatat atcgacgatg ttcgatttat tttaagggtt 240

gaaatttacg ggtttgagag attataagag cgttttttat cgttatggaa taacggggat 300

agaacgtttc ggtcgtttcg gggggttcgga aaaggtacgg tttaggattt agggaggcgc 360

ggggagttag gtttgggttt cgggttttta agatttttgt gttcgttgtc gtcgcggttt 420

tgttgttggt gagttttcgt cgcggttttt ggttggggaa gagcgtgttt ggcgtttgga 480

gagggtaggg agagaggggg atacggcggg ggtgcgtggt tcgggtcgtt tgcggtcggg 540

tatgttcggg taagacgtat tagtcgtcgg agtcggggga agagatgggt tttcgggttg 600

ggtaggagcg atttgggtcg ttagggaata gagcgcgcgt tttatttggt gtaaattttc 660

-continued

gaatttagtg ggggagggcg ataaggaggg aattttcgag taagttgcgt gaagttacgg 720

agaggtcgtc ggattttgat tttgtttttt tttttatttt tttgtttttt tttttttttt 780

tttttttttt tttttttttt tttttttttt tttcgtttag tttttgtttt aatttttttt 840

ttttttgcgt tttcgaatga atttttaaag gcgtttattg tagatcgttt tgaatttgcg 900

gtcggcgaag aatttttttg tggtcgttgc ggtttagtgg tttcgtttcg tgcgcgggag 960

tcgtcgcggg cgtagttgga gaggtttttt tttttttta gcggttgcgt ttttacgcgt 1020

gcggggtcgt ttatcgttaa tgttattgtt tggggttttt tgggaaaacg agatttagga 1080

gaagggagtt gtggtatttg 1100

<210> SEQ ID NO 48
<211> LENGTH: 1048
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48

taagtgttat aatttttttt ttttaaattt cgttttttta aggaatttta aataatggta 60

ttggcgatga gcggtttcgt acgcgtaggg gcgtagtcgt taaggagggg aaggggtttt 120

tttagttgcg ttcgcgacga ttttcgcgta cggaacggaa ttattgggtc gtagcgatta 180

taggggagtt tttcgtcggt cgtaggttta aagcgatttg taatgagcgt ttttaggaat 240

ttattcgaag gcgtaaaaga aaaagaaatt aaggtaggaa ttgagcgagg aaggaaggga 300

gggaaagaaa ggaagaaaga gaaaaagaga aagaaataga aagtaaggaa agaaaataaa 360

attaaagttc gacgattttt tcgtggtttt acgtagttta ttcgggaatt tttttttgt 420

cgtttttttt tattggattc gggaatttat attaagtgga gcgcgcgttt tgtttttttgg 480

cggtttaggt cgtttttgtt taattcgggg atttattttt tttttcgatt tcgacgattg 540

gtgcgttttg ttcggatatg ttcggtcgta ggcgattcgg gttacgtatt ttcgtcgtgt 600

tttttttgc ggggatttat taatagtagg atcgcggcga taacgagtat aagggttttg 660

gggattcggg gtttaggttt ggtttttcgc gtttttttgg gttttgggtc gtgttttttt 720

cgggttttcg aagcggtcgg ggcgttttgt tttcgttgtt ttatggcggt agggaacgtt 780

tttatagttt tttaggttcg tgggttttag tttttaaagt agatcgggta tcgtcggtgt 840

atttgtggg cgtagagatt gcggggtttt tcggtcgcgt gttgatttat gtgtttaggt 900

tgatttgggg cggcgcggtt gtatttttat tgttttcggg taggcgttat tcggggcggg 960

gcgaattaga tttaatgtgt aattgtaaat tttattatag gttggtgata ataaataaga 1020

gtttcgttaa cgtaattttt cgtaagcg 1048

<210> SEQ ID NO 49
<211> LENGTH: 1299
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 49

tgtacgttta ttgtttgttt tttttttgt acgtttggtg ggttttattt taggcgggtg 60

ttgcgacggt ggttattgcg tttttgcgta cgcgggggta gttttcgtcg ttattttttt 120

tggcgtatat gttgagtttt tatcgcgatt cgttgtcgag ggtagatatt attcgtagtt 180

tataggtaga aggtaggtag tgtcgcgtgt cgcgttttgt tgggtatttt cggggcgttt 240

tcgtcgcgtt tagttagcgg attcgggaag tgttgtgggt tgggggttgc ggtttcgagt 300

cgggtttgta gtcgttcggg cgtttcgagt ttagggttta gttttgcggg tgttttcgcg 360

-continued

ttagtaggtt cggggtgtag cgttggtggt tgggggcgta tttacggtcg agtcgggaag 420

ggattttagc gtttagggtg tgttttcgac ggggattatt gtttttgggt tttggtttgg 480

gattgcgcgg agcgtagcgc ggaagggtgg gagtttttaa tttttagttt tgtgaagttg 540

tttatttcgg agtttgggtt tgcgtatttg taggataggt gtaataaata atatttcgtt 600

tattagattg tggaaagcgc gagatgataa tgcgcgcgaa acgtttagcg tagtattcgg 660

tatagttata gttaacggtc gttggtatta ttgtaatggt ttggttttgg cgcgggagta 720

tcggtagttg agttggtaat atcggggatt cgggtttacg gttcggagat tagggatggg 780

ttgtttcgaa gtcgcgaatt gtggtagttt tgggtttttt agtcgcgtcg gggaagtgtt 840

aagtgtttcg tttaatttcg ggttcggggt tatgatttgt aggggagtgg gtgttaagga 900

cggtagggat ttgagggtat cgttttcgag gatttggtag cgcgttttgg gtatttagcg 960

cggcgagtag gtgggtgttg cggagaggga gtttttttcg cgttttaatt tatattttgt 1020

cgtttgggta gtcgcggtcg tttacgtttt ttttcgtttg cgggggttag acggtttttt 1080

ttggggtcgg ggcgtaattt ataaacgtta atttgattcg atttgtcgtt tgttcgtttt 1140

ttgtgatttg gtgtcggggg tttttcgttt tcgcgtttgg ggttagatag tcggtgattt 1200

ttttcggaag ggttatttgg ggattagtta gattagggga tattttcggg ggcggggtaa 1260

tgagaaattt gttggagtgt tcggtttttt aatcgaaaa 1299

<210> SEQ ID NO 50
<211> LENGTH: 1350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 50

ttttcggttg aggggtcgag tattttagta aatttttttat tgtttcgttt tcgagggtgt 60

tttttggttt ggttggtttt tagatgattt tttcggagag ggttatcggt tgtttgattt 120

taggcgcggg agcgaagggt tttcggtatt aggttataag gggcgggtag gcggtaggtc 180

ggattagatt agcgtttgtg gattgcgttt cggttttagg gagggtcgtt tggttttcgt 240

aggcggaggg aggcgtgggc ggtcgcggtt gtttaggcgg tagaatgtgg attgaggcgc 300

ggaaggggtt tttttttcgt agtatttatt tgttcgtcgc gttgggtgtt tagaacgcgt 360

tgttaggttt tcgagggcga tatttttaga tttttgtcgt ttttgatatt tattttttttg 420

taaattatgg tttcgaattc ggggttaagc gagatatttg atattttttc ggcgcggttg 480

gaggatttaa ggttgttata gttcgcgatt tcgggatagt ttatttttga ttttcgggtc 540

gtgagttcga attttcgatg ttattagttt agttgtcgat attttcgacg ttatatttcg 600

ggatttattt atttttattc gtagaaagaa aaaaaaatcg ttaagattaa attattatag 660

taatattaac gatcgttgat tgtggttgtg tcgggtattg cgttgagcgt ttcgcgcgta 720

ttgttatttc gcgtttttta tagtttgata ggcgaggtgt tatttattat atttatttta 780

tagatgcgta gatttaggtt tcgggataag taattttata agattggaga ttagaagttt 840

ttattttttc gcgttgcgtt tcgcgtaatt ttaaattaaa atttagagat aatggttttc 900

gtcgaggata tattttgaac gttagaattt tttttcgatt cggtcgtgga tacgttttta 960

gttattaacg ttgtatttcg agtttgttga cgcggagata ttcgtagagt taggttttgg 1020

gttcgggacg ttcgggcggt tgtaaattcg gttcggagtc gtagttttta atttatagta 1080

tttttcgagt tcgttggttg gacgcggcgg aggcgtttcg gggtgttta gtagggcgcg 1140

gtacgcggta ttgtttattt tttgtttgta ggttgcggat gatgtttgtt ttcggtagcg 1200

-continued

ggtcgcggta gaggtttagt atgtacgtta gaggggatgg cgacgagggt tgttttcgcg 1260

tacgtaggag cgtagtggtt atcgtcgtag tattcgtttg gagtagggtt tattaggcgt 1320

gtagaaggaa gggtaggtag tgggcgtgta 1350

<210> SEQ ID NO 51
<211> LENGTH: 350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 51

ttttgaaggg cggcggattt tagggttatg ttggttgttt ttagaaagta ggagttcgaa 60

atcgcggggt taacgaacgt ttatattttt tgttataatt tcgttatttt tttgcgtttt 120

tttttttgtt ttttgttttt ataggtaacg tttagaacga gtgttttttt cggtggggta 180

ttgaggagtt tgggttgtag ttgtcgagtc gttatagtta cgttgagttc ggtttggttt 240

gtatattggc gttatcgttt ggcggggagc gggattgacg cgtttttttt tttttttttt 300

agtttagatt acggaggcgc ggagttttat tttttgtttt gggcgagggg 350

<210> SEQ ID NO 52
<211> LENGTH: 350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

tttttcgttt agggtaggag atggagtttc gcgttttcgt gatttgggtt ggaggagagg 60

gagaggagcg cgttagtttc gtttttcgtt aggcggtggc gttagtgtgt aggttaggtc 120

gggtttagcg tggttgtggc ggttcggtag ttgtagttta ggttttttag tattttatcg 180

ggagaagtat tcgttttggg cgttatttgt gggggtaggg ggtaagggga gaggcgtagg 240

ggagtggcga ggttgtagta gagaatgtgg gcgttcgttg gtttcgcggt ttcgggtttt 300

tgtttttttgg ggatagttag tatggttttg aagttcgtcg tttttttagag 350

<210> SEQ ID NO 53
<211> LENGTH: 350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

taattagggt tggtttattt ttttttagtt aatttttttt tatttttagt ttttaattta 60

atttatttcg tttattagtt tttggatttt tattattttt ttcgtatttt cggtagtttt 120

ggggaagttt cgtgacgtta taggtttcgt ttttagtttc ggttcggggt tagtgcgtgt 180

tgacgttatg ttgcgtgcgg gtcggtgcgg aatcgttttt ttaatttcgc ggggtagtag 240

gagttagtta gtaaagagtc gaggtcgggc gcgcgatttt cgtttttttg tttttggtcg 300

tatattttgc gtatattttt tttttgtat ggtggatatt attttttatt 350

<210> SEQ ID NO 54
<211> LENGTH: 350
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54

aatgaaaaat aatatttatt atgtagaaaa agagatgtgc gtaaagtgtg cggttagggg 60

tagaaggacg agggtcgcgc gttcggtttc ggttttttgt taattaattt ttattgtttc 120

gcggagttga aggagcgatt tcgtatcggt tcgtacgtag tatgacgtta atacgtatta 180

-continued

```
gtttcgggtc ggagttgggg gcgggatttg tggcgttacg aagttttttt agaattgtcg    240

gggatgcggg ggaggtgatg gggatttagg ggttgatggg cggggtgggt tgggttggag    300

gttgggggtg aagggagatt ggttgggagg aagtgggtta attttgattg               350


<210> SEQ ID NO 55
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 55

gagcgggtag cgagagtttc gg                                              22


<210> SEQ ID NO 56
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 56

taacgacgcg actaccgaaa acc                                             23


<210> SEQ ID NO 57
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 57

gattaacgtg ttcgtgattt cgtt                                            24


<210> SEQ ID NO 58
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 58

caacgaccaa taaccaatca acgcc                                           25


<210> SEQ ID NO 59
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 59

atacgtcggt gagttcggtt tatc                                            24


<210> SEQ ID NO 60
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 60

actcccgact ccctaaactc cgaa                                            24


<210> SEQ ID NO 61
```

```
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 61

tgaatcggcg aggtgagagt cg                                                22


<210> SEQ ID NO 62
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 62

accgaacgtc tcaacgcgaa aacg                                              24


<210> SEQ ID NO 63
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 63

tatcgttagc gtcgtggtgg agtt                                              24


<210> SEQ ID NO 64
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 64

ctacacgaac actaaaccga ccga                                              24


<210> SEQ ID NO 65
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 65

tcggtcgtta cgttgatcgt tattc                                             25


<210> SEQ ID NO 66
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 66

accctacgca tacccttctc gaac                                              24


<210> SEQ ID NO 67
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 67
```

```
gtttcgagga agtttcgggt acgg                                              24


<210> SEQ ID NO 68
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 68

gatcgttaac cttctttcgc cgac                                              24


<210> SEQ ID NO 69
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 69

cgaagttggg aggagcgagt t                                                 21


<210> SEQ ID NO 70
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 70

aaacatccgt actcctacga ccga                                              24


<210> SEQ ID NO 71
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 71

cgtattagtc gtattcgcga gcgt                                              24


<210> SEQ ID NO 72
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 72

cgaaactact cgacccgacc c                                                 21


<210> SEQ ID NO 73
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 73

taacggtacg ttggaggtcg agtt                                              24


<210> SEQ ID NO 74
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
```

```
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 74

acgaccgcct ccttaaacta cgct                                               24


<210> SEQ ID NO 75
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 75

tatcgtgtat tcgttgcggt tagg                                               24


<210> SEQ ID NO 76
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 76

aacgatacga acgacgtacc gaa                                                23


<210> SEQ ID NO 77
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 77

tacgtgaata agaggacgtt tcgg                                               24


<210> SEQ ID NO 78
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 78

aacgatcttc cgaaatacgc caa                                                23


<210> SEQ ID NO 79
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 79

tcgtcgaatc ggtatcgtcg tc                                                 22


<210> SEQ ID NO 80
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 80

acctatatcc acgtcccgaa acct                                               24


<210> SEQ ID NO 81
```

<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 81

cggttgtagt ttgttcgttc gtttc 25

<210> SEQ ID NO 82
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 82

ctaacgcctc ataactcctc gcgt 24

<210> SEQ ID NO 83
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 83

gcgtcgattc gggagtagta tcgt 24

<210> SEQ ID NO 84
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 84

ataccgtaaa tccgcgctac ttcc 24

<210> SEQ ID NO 85
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 85

cgttgaggtc gaatgaagcg tagt 24

<210> SEQ ID NO 86
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 86

aaccgaaact aaacacgacg caa 23

<210> SEQ ID NO 87
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 87

```
aagcgtatag ttcgaggatt gcga                                             24


<210> SEQ ID NO 88
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 88

ccgcgtcact tactcctcta cga                                              23


<210> SEQ ID NO 89
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 89

cgttgggtgc gtaggaaggt tagt                                             24


<210> SEQ ID NO 90
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 90

gaccgaccct aaacaacccg ct                                               22


<210> SEQ ID NO 91
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 91

gttgcgggat agcgttgtga tt                                               22


<210> SEQ ID NO 92
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 92

accattatca atactccgat cgcc                                             24


<210> SEQ ID NO 93
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 93

tttgtttgtt aagggcgtta tcgt                                             24


<210> SEQ ID NO 94
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
```

```
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 94

ccgcgactac tctaaccaac cc                                              22


<210> SEQ ID NO 95
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 95

gggcgttgag tttagttcgg aga                                             23


<210> SEQ ID NO 96
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 96

acgaacacaa ccgaatcaac gtaa                                            24


<210> SEQ ID NO 97
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 97

ggcgttggtt gttagagcga tg                                              22


<210> SEQ ID NO 98
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 98

gactcaaact cactcaccga cgac                                            24


<210> SEQ ID NO 99
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 99

ggtgcgattt aggatttagg acgg                                            24


<210> SEQ ID NO 100
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 100

gcgaccgaaa ctcactaaca acaa                                            24


<210> SEQ ID NO 101
```

```
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 101

gcgatttggg tcgttaggga atag                                            24


<210> SEQ ID NO 102
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 102

acctctccgt aacttcacgc aactt                                           25


<210> SEQ ID NO 103
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 103

ggtagtcgcg gtcgtttacg tt                                              22


<210> SEQ ID NO 104
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 104

acgaacaaac gacaaatcga atca                                            24


<210> SEQ ID NO 105
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 105

tacgttgagt tcggtttggt ttgt                                            24


<210> SEQ ID NO 106
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 106

cgcgcctccg taatctaaac taa                                             23


<210> SEQ ID NO 107
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 107
```

```
gtgcgtgttg acgttatgtt gcgt                                        24


<210> SEQ ID NO 108
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 108

cgcccgacct cgactcttta ct                                          22


<210> SEQ ID NO 109
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 109

cggcgatttc ggggatttta gggc                                        24


<210> SEQ ID NO 110
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 110

gaccgctctt ctaaaaaatc ccgcg                                       25


<210> SEQ ID NO 111
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 111

acgttcgggg tgtagcggtc gtc                                         23


<210> SEQ ID NO 112
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 112

ccccaatact aaatcacgac gccg                                        24


<210> SEQ ID NO 113
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 113

ggtcggcgtc gtgatttagt attgg                                       25


<210> SEQ ID NO 114
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
```

<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 114

actacgacga cgaaactcca acga 24

<210> SEQ ID NO 115
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 115

tgtggtgatt ttggggattt tagggt 26

<210> SEQ ID NO 116
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 116

ccaaccactc ttctaaaaaa tcccaca 27

<210> SEQ ID NO 117
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 117

gatgtttggg gtgtagtggt tgttg 25

<210> SEQ ID NO 118
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 118

ctccacccca atactaaatc acaaca 26

<210> SEQ ID NO 119
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 119

gtcaggtggg ctactccacc agggaggcct tctccccacc cctggcccag ggcccttccg 60

gatttccaga gaattctgga accaagacct tcccctttct caccagggac ctccttgctc 120

cagggcctcc cgagcgcctg gccgtgaggc agggcccaga aggccagggc gggatccagg 180

tggctggcct cacccactgg gacgtgccca acctggagac attgcaccag gtagggctgc 240

accgctctcc gagaccccgc cccgtgcttc cacttggggg cggggaccct gcacctgacc 300

agcccttcgc cccgccttcc agatgctgaa actggggagg agcaaccggg ccaccgccgc 360

caccgccatg aaccagcgca gctcccgctc gcatgccctg gtcacgctga cgctgcgcgc 420

ggcgtctcca ccgcgcgctc caggcaccgc aggtaccacg gccggtgcct gagccctgcg 480

gagtctccag agcacccgag gcccggcctt cccccatgtc gggctcgctc gcccctctag 540

-continued

```
gcacgctgca cctggtggac ctggcgggat ccgaacgcgc acggaaggca ggggcggccg    600

gcccgccgcg gggagaccca gacggcgccc ggcgcctgcg ggaggcccag accataaacc    660

gctcgctgct ggcgctagga ggcgtgatgg ccgcactgcg ggcccaccgg ccgcacgtgc    720

ccttccgcga ctcgcagctc acgcgactgc tgcagccggc gctgggccca ggcaccaccg    780

cggtgctgct gctgcaggtg ggcgccgggg cggggcaggt gtgtgcgtgc cggtcgccgc    840

ccacccgggc ccgcccaccc gcgcctcttg cccgcagatc tccacgcggc cggaggatct    900

cggggagaca gtctgctccc tcaagttcgc cgaccgagtg ggtcaagtgg agctggggcc    960

agcccggcgc cgcagggtcc cgcgctcctc cgggacgcct tcttccctca gcaccgacac   1020

tccgctcacc gggacccct gcacccctac gccgtcccct ggcagtcctc catgccccag   1080

tcccgacaac ggctcgggct cggctctcgc gcccgcagag ggcctgcccc tctagtcctg   1140

ggtcgcggcc ctgcccatgg ggtctcaggc caggtctctg ctggcagagg cggtagtaaa   1200

gtccctgtac cccgtctccc agggcacaag ctccctagcc tctttggatc cattgcccct   1260

gagctcccag agtcacccct ccacctccgc agccagtgaa                         1300


<210> SEQ ID NO 120
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 120

ttcactggct gcggaggtgg aggggtgact ctgggagctc aggggcaatg gatccaaaga     60

ggctagggag cttgtgccct gggagacggg gtacagggac tttactaccg cctctgccag    120

cagagacctg gcctgagacc ccatgggcag ggccgcgacc caggactaga ggggcaggcc    180

ctctgcgggc gcgagagccg agcccgagcc gttgtcggga ctggggcatg gaggactgcc    240

aggggacggc gtaggggtgc agggggtccc ggtgagcgga gtgtcggtgc tgagggaaga    300

aggcgtcccg gaggagcgcg ggaccctgcg gcgccgggct ggccccagct ccacttgacc    360

cactcggtcg gcgaacttga gggagcagac tgtctccccg agatcctccg gccgcgtgga    420

gatctgcggg caagaggcgc gggtgggcgg gcccgggtgg gcggcgaccg gcacgcacac    480

acctgccccg ccccggcgcc cacctgcagc agcagcaccg cggtggtgcc tgggcccagc    540

gccggctgca gcagtcgcgt gagctgcgag tcgcggaagg gcacgtgcgg ccggtgggcc    600

cgcagtgcgg ccatcacgcc tcctagcgcc agcagcgagc ggtttatggt ctgggcctcc    660

cgcaggcgcc gggcgccgtc tgggtctccc cgcggcgggc cggccgcccc tgccttccgt    720

gcgcgttcgg atcccgccag gtccaccagg tgcagcgtgc ctagaggggc gagcgagccc    780

gacatggggg aaggccgggc ctcgggtgct ctggagactc cgcagggctc aggcaccggc    840

cgtggtacct gcggtgcctg gagcgcgcgg tggagacgcc gcgcgcagcg tcagcgtgac    900

cagggcatgc gagcgggagc tgcgctggtt catggcggtg gcggcggtgg cccggttgct    960

cctccccagt ttcagcatct ggaaggcggg gcgaagggct ggtcaggtgc agggtccccg   1020

cccccaagtg gaagcacggg gcggggtctc ggagagcggt gcagccctac ctggtgcaat   1080

gtctccaggt tgggcacgtc ccagtgggtg aggccagcca cctggatccc gccctggcct   1140

tctgggccct gcctcacggc caggcgctcg ggaggccctg gagcaaggag gtccctggtg   1200

agaaagggga aggtcttggt tccagaattc tctggaaatc cggaagggcc ctgggccagg   1260

ggtggggaga aggcctccct ggtggagtag cccacctgac                         1300


<210> SEQ ID NO 121
```

<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 121

aacacgtgta ggttgttgga attacattaa cgaatgaatg agcaaaacct tctaaaccac 60

cgaccaatga aaccccgata cagaaaatcg ctgtcatgag taagttagca ctcctgaaga 120

gtttgaatac tgaactggcc agagtctgcg cgccgacgcc ccccaggtgg ccggagtgac 180

ccggagcagg cgtggctgtc tctcagaccc gcgcgttggg cccgaacagt ttgtccccac 240

gcagctccca tataaggcgg gcccctcccc tgccccagcc agctaggtcg ccgcgctggc 300

tccctggcgg cttctcaaac caacccgccg ctactgcgca tgcttggcaa gctcgcccgc 360

tccttaatat cctgctccgg ctgttcctgc cacccgttgg tcaaattcgc acccagctct 420

gctccagaca gagggaaaac ccagtgattt ccgggctcta gaaacaaagg gaggctatga 480

ttccctgctg gccctagggg tccagggaag gttatggaaa gataattctt tgtgtaagcg 540

ggttgcgtac 550

<210> SEQ ID NO 122
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 122

gtacgcaacc cgcttacaca aagaattatc tttccataac cttccctgga cccctagggc 60

cagcagggaa tcatagcctc cctttgtttc tagagcccgg aaatcactgg gttttccctc 120

tgtctggagc agagctgggt gcgaatttga ccaacgggtg gcaggaacag ccggagcagg 180

atattaagga gcgggcgagc ttgccaagca tgcgcagtag cggcgggttg gtttgagaag 240

ccgccaggga gccagcgcgg cgacctagct ggctggggca ggggaggggc ccgccttata 300

tgggagctgc gtggggacaa actgttcggg cccaacgcgc gggtctgaga gacagccacg 360

cctgctccgg gtcactccgg ccacctgggg ggcgtcggcg cgcagactct ggccagttca 420

gtattcaaac tcttcaggag tgctaactta ctcatgacag cgattttctg tatcggggtt 480

tcattggtcg gtggtttaga aggttttgct cattcattcg ttaatgtaat tccaacaacc 540

tacacgtgtt 550

<210> SEQ ID NO 123
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 123

cagccgaggg gcgcgcctgg ctgatgtgtg gttgaatgga gagcggccca accctcctcc 60

ttcctcctct tcttctcccc gccctgacac ccgggcctca aacttcaacc aaagcccgtg 120

ccctttttcaa tttacccccc tcgatcaaaa tgagccattc ttgtctgtcc tccgcggcgg 180

cccattgtct ggcgtgatag gtttgcagat ttgacagctg ggcgcacgca gatttgattc 240

aaactcggtc tccccgagag atgaacttgg acatcagcaa agatcccgag cactgccggc 300

tggctcctag accggtctcc cgacccagtg tagacttcgg tgccccgggc gcccccggc 360

gtgcgggaag gggagcgtgt gtcaggcgtg gggggcgggg ggtgagcagc acgactggga 420

accagcggtc ccaggggttg gggcgaaggg ctgtgtacat gttaggcttt ttttgttgtt 480

gttaatttac tctcgaaaca gccaaaatgg aggtcagctt ataaattttc taaagccagg 540 tctggccggg 550

<210> SEQ ID NO 124
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 124

cccggccaga cctggcttta gaaaatttat aagctgacct ccattttggc tgtttcgaga 60

gtaaattaac aacaacaaaa aaagcctaac atgtacacag cccttcgccc caacccctgg 120

gaccgctggt tcccagtcgt gctgctcacc ccccgccccc cacgcctgac acacgctccc 180

cttcccgcac gccgggggc gcccggggca ccgaagtcta cactgggtcg ggagaccggt 240

ctaggagcca gccggcagtg ctcgggatct ttgctgatgt ccaagttcat ctctcgggga 300

gaccgagttt gaatcaaatc tgcgtgcgcc cagctgtcaa atctgcaaac ctatcacgcc 360

agacaatggg ccgccgcgga ggacagacaa gaatggctca ttttgatcga gggggtaaa 420

ttgaaaaggg cacgggcttt ggttgaagtt tgaggcccgg gtgtcagggc ggggagaaga 480

agaggaggaa ggaggagggt tgggccgctc tccattcaac cacacatcag ccaggcgcgc 540

ccctcggctg 550

<210> SEQ ID NO 125
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 125

agaaactgag gtcggagtgg gggcgtgacc aggccagcct aaggccgctg cactaatgag 60

aagctgagct ctcagatttt tgcctccctg tccctgccaa gtcgctgttt cctgggacaa 120

gagggagcct cactgaaacg aactccggtc tcaggggaca gaatcctgaa accctggctc 180

tggggtccgg ggcaggggtg cgctgcctca ggacagacgg tgaaactgag gtccagagcc 240

ggacatccac cgcctgcgga gggaacgaga acgcggcgcg tcctgccttg cgggccgagc 300

ggcgccagag ccgcctcctc ccgcccccg cgctagatcc ccccgccccg tctttgccct 360

cgcgacgccg ccacctccgg aacaagccat ggtggcggcg acggtggcag cggcgtggct 420

gctcctgtgg gctgcggcct gcgcgcagca ggagcaggac ttctacgact tcaaggcggt 480

caacatccgg ggcaaactgg tgtcgctgga gaagtaccgc ggatcggtga gtgcgcgggg 540

tctggcggcg ccgctgggcc cggcctcgcc ctggcggggc ctgctgggga cgccccgcag 600

cccggtcccc cgcgcggtgt ggctccgagg acgctccagc cgcgcggccg ccaaaccccg 660

gcccccgccc cgctcggccg tgacctctgg cgcggcgccc ccatcccgcg cccggcccgg 720

cccggcccgc ggctacgtgg cacggccttg gcgcggagga acccgaagcg ctcgcagtcg 780

gcgcccactt cgctaccggc acctttgggc agcggggtcc agaccttcgc cgggaggccg 840

ggcaccactg cccagccttt gccattcacg ggtgaaaaaa gtaaccgtag catcgtgcgg 900

cctttccctc tcccgtcctc attttctgca tctggaacgg ggagtggctg attcggagtc 960

cagtgaagaa cactgtggag atcaatgtgc agggcagaga gagagttatt tcagatgcac 1020

ggagacctca cacggatcat ccctgggaga 1050

<210> SEQ ID NO 126
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 126

tctcccaggg atgatccgtg tgaggtctcc gtgcatctga aataactctc tctctgccct 60

gcacattgat ctccacagtg ttcttcactg gactccgaat cagccactcc ccgttccaga 120

tgcagaaaat gaggacggga gagggaaagg ccgcacgatg ctacggttac ttttttcacc 180

cgtgaatggc aaaggctggg cagtggtgcc cggcctcccg gcgaaggtct ggaccccgct 240

gcccaaaggt gccggtagcg aagtgggcgc cgactgcgag cgcttcgggt tcctccgcgc 300

caaggccgtg ccacgtagcc gcgggccggg ccgggccggg cgcgggatgg gggcgccgcg 360

ccagaggtca cggccgagcg gggcgggggc cggggtttgg cggccgcgcg gctggagcgt 420

cctcggagcc acaccgcgcg ggggaccggg ctgcggggcg tccccagcag gccccgccag 480

ggcgaggccg ggcccagcgg cgccgccaga ccccgcgcac tcaccgatcc gcggtacttc 540

tccagcgaca ccagtttgcc ccggatgttg accgccttga agtcgtagaa gtcctgctcc 600

tgctgcgcgc aggccgcagc ccacaggagc agccacgccg ctgccaccgt cgccgccacc 660

atggcttgtt ccggaggtgg cggcgtcgcg agggcaaaga cggggcgggg ggatctagcg 720

cggggggcgg gaggaggcgg ctctggcgcc gctcggcccg caaggcagga cgcgccgcgt 780

tctcgttccc tccgcaggcg gtggatgtcc ggctctggac ctcagtttca ccgtctgtcc 840

tgaggcagcg caccccctgcc ccggacccca gagccagggt ttcaggattc tgtcccctga 900

gaccggagtt cgtttcagtg aggctccctc ttgtcccagg aaacagcgac ttggcaggga 960

cagggaggca aaaatctgag agctcagctt ctcattagtg cagcggcctt aggctggcct 1020

ggtcacgccc ccactccgac ctcagtttct 1050

<210> SEQ ID NO 127
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 127

ttctcttacg atctggcttt actctcacgc gcacagccga gtccctgggg acccagcaga 60

ggtccgaagc ggagcggggc ggggcggggc tacggaagct ggcgaggccg agcccctcct 120

agtgcttccg gaccttgctc cctgaacact cggaggtggc ggtggatctt actccttcca 180

gccagtgagg atccagcaac ctgctccgtg cctcccgcgc ctgttggttg gaagtgacga 240

ccttgaagat cggccggttg gaagtgacga ccttgaagat cggcgggcgc agcggggccg 300

agggggcggg tctggcgcta ggtccagccc ctgcgtgccg ggaaccccag aggaggtcgc 360

agttcagccc agctgaggcc tgtctgcaga atcgacacca accagcatca tgtccatgac 420

actggggtac tgggacatcc gcggggtgag tgagggtccg ctgcactgtg ggaccgggcg 480

cgtgggcggg aagtgccgag cggctgggga ccggctctag ggacggttcc ctccttaggg 540

ctatctctca 550

<210> SEQ ID NO 128
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 128

tgagagatag ccctaaggag ggaaccgtcc ctagagccgg tccccagccg ctcggcactt 60

cccgcccacg cgcccggtcc cacagtgcag cggaccctca ctcaccccgc ggatgtccca 120

gtaccccagt gtcatggaca tgatgctggt tggtgtcgat tctgcagaca ggcctcagct 180

-continued

gggctgaact gcgacctcct ctggggttcc cggcacgcag gggctggacc tagcgccaga 240

cccgcccccct cggccccgct gcgcccgccg atcttcaagg tcgtcacttc caaccggccg 300

atcttcaagg tcgtcacttc caaccaacag gcgcgggagg cacggagcag gttgctggat 360

cctcactggc tggaaggagt aagatccacc gccacctccg agtgttcagg gagcaaggtc 420

cggaagcact aggaggggct cggcctcgcc agcttccgta gccccgcccc gccccgctcc 480

gcttcggacc tctgctgggt ccccagggac tcggctgtgc gcgtgagagt aaagccagat 540

cgtaagagaa 550

<210> SEQ ID NO 129
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 129

tcttgaattg ggggcggagg taaaaaaaaa aaaaaagtcc tcactgtggg aagctataaa 60

aagcaaagag gactggggag agagcagaga gagagaaagc gggagcccgc ggcgagcgta 120

gcgcaagtcc gctccctagg catcgctgcg ctggcagcga ttcgctgtct cttgtgagtc 180

aggggacaac gcttcggggc aactgtgagt gcgcgtgtgg gggacctcga ttctcttcag 240

atctcgagga ttcggtccgg ggacgtctcc tgatccccta ctaaagcgcc tgctaacttt 300

gaaaaggagc actgtgtcct gcaaagtttg acacataaag gataggaaaa gagaggagag 360

aaaagcaact gagttgaagg agaaggagct gatgcgggcc tcctgatcaa ttaagaggag 420

agttaaaccg ccgagatccc ggcgggacca aggaggtgcg ggcaagaag gaacggaagc 480

ggtgcgatcc acagggctgg gttttcttgc accttgggtc acgcctcctt ggcgagaaag 540

cgcctcgcat 550

<210> SEQ ID NO 130
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 130

atgcgaggcg ctttctcgcc aaggaggcgt gacccaaggt gcaagaaaac ccagccctgt 60

ggatcgcacc gcttccgttc cttcttgccc cgcacctcct tggtcccgcc gggatctcgg 120

cggtttaact ctcctcttaa ttgatcagga ggcccgcatc agctccttct ccttcaactc 180

agttgctttt ctctcctctc ttttcctatc ctttatgtgt caaactttgc aggacacagt 240

gctccttttc aaagttagca ggcgctttag taggggatca ggagacgtcc ccggaccgaa 300

tcctcgagat ctgaagagaa tcgaggtccc ccacacgcgc actcacagtt gccccgaagc 360

gttgtcccct gactcacaag agacagcgaa tcgctgccag cgcagcgatg cctagggagc 420

ggacttgcgc tacgctcgcc gcgggctccc gctttctctc tctctgctct ctccccagtc 480

ctctttgctt tttatagctt cccacagtga ggactttttt ttttttttta cctccgcccc 540

caattcaaga 550

<210> SEQ ID NO 131
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 131

cgattggctg caagggtctc ggcttggccg cggattggtc acacccgagg gcttgaaagg 60

-continued

tggctgggag cgccggacac ctcagacgga cggtggccag ggatcaggca gcggctcagg 120

cgaccctgag tgtgccccca ccccgccatg gcccggctgc tgcaggcgtc ctgcctgctt 180

tccctgctcc tggccggctt cgtctcgcag agccggggac aagagaagtc gaaggtgagt 240

gagcctccgg gccgggggcc gggagaaaaa acctagcccc tcggtgtcca gcgctcagtg 300

caatgcaccc cttttcccag gctccccgcc agatgggcaa tccccaggtg cgagagacct 360

cctgaacccc ttttgccgcc ccctccgccg ccgggacccc gcccccgacc gtcgtcgtct 420

cgtagttcca tctgttggag agccgagacc tggtgcttca ggcgggcaga atgactaagg 480

gaggaaggtc tctctccccg agctcgcact ttctccccac tgccacctcg agggtcgcct 540

tgctacatct 550

<210> SEQ ID NO 132
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 132

agatgtagca aggcgaccct cgaggtggca gtggggagaa agtgcgagct cggggagaga 60

gaccttcctc ccttagtcat tctgcccgcc tgaagcacca ggtctcggct ctccaacaga 120

tggaactacg agacgacgac ggtcgggggc ggggtcccgg cggcggaggg ggcggcaaaa 180

ggggttcagg aggtctctcg cacctgggga ttgcccatct ggcggggagc ctgggaaaag 240

gggtgcattg cactgagcgc tggacaccga ggggctaggt tttttctccc ggcccccggc 300

ccggaggctc actcaccttc gacttctctt gtccccggct ctgcgagacg aagccggcca 360

ggagcaggga aagcaggcag gacgcctgca gcagccgggc catggcgggg tgggggcaca 420

ctcagggtcg cctgagccgc tgcctgatcc ctggccaccg tccgtctgag gtgtccggcg 480

ctcccagcca cctttcaagc cctcgggtgt gaccaatccg cggccaagcc gagacccttg 540

cagccaatcg 550

<210> SEQ ID NO 133
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 133

aggggaactg gtatctccac agtaattact agagcagctc tggggaacgg agggttggct 60

aaggaagaaa agctccccca acccttgggg cgagggagcg ttctctcaat ggagcccccc 120

caactcccct ccacccccca ccagtcttcc aggaaagagg aataccctac ccggcagggc 180

tgcgaaggaa ggggaaatcc aaccagagcg aaagtcgcac gcggacagct ctgccagccc 240

ttggaggcat ccggcggtca cccacgggac aaagcgcggc tgcgggagcg cgcgcggggc 300

attccggacc cgcgtcgagc tccgctctag agggggcggc gggcggcgac aagccggaga 360

gaggaagggc caaggagcac ggccctcctg tcggcaccat cagcgggaga gtggcgagcg 420

gacgcctaga cggaggggcc ctactcagac cccatcgagc cagttcccaa gcttttccct 480

ccgacctgct ccctcccggg gcgcgtgagg gtgcgggtcg ggggtgaacc tggtgttggg 540

gaaagtgatt 550

<210> SEQ ID NO 134
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 134

aatcactttc cccaacacca ggttcacccc cgacccgcac cctcacgcgc cccgggaggg 60

agcaggtcgg agggaaaagc ttgggaactg gctcgatggg gtctgagtag ggcccctccg 120

tctaggcgtc cgctcgccac tctcccgctg atggtgccga caggagggcc gtgctccttg 180

gcccttcctc tctccggctt gtcgccgccc gccgccccct ctagagcgga gctcgacgcg 240

ggtccggaat gccccgcgcg cgctcccgca gccgcgcttt gtcccgtggg tgaccgccgg 300

atgcctccaa gggctggcag agctgtccgc gtgcgacttt cgctctggtt ggatttcccc 360

ttccttcgca gccctgccgg gtagggtatt cctctttcct ggaagactgg tgggggtgg 420

aggggagttg gggggctcc attgagagaa cgctccctcg ccccaagggt tgggggagct 480

tttcttcctt agccaaccct ccgttcccca gagctgctct agtaattact gtggagatac 540

cagttcccct 550

<210> SEQ ID NO 135
<211> LENGTH: 2800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 135

cgggcaaaaa tggagagcag gcagaggtca catcctcctc ctcttcctca cgctcccggg 60

ctgcgtgccc acaggggcac agccctgtgc gcggtgccac cgggggccat caggctgggt 120

tagaggaagg cccgacctcc gcgcagcaaa gaaaacaaac acagatgtgt ttggctggga 180

ccgggaggga gaaagtggcc cccttccccc gcccgcgcgc tcccccgggc gtgaggctct 240

ccgggcggcg cggggcgcgg gcgaggctga cagtccccgg cggcccctcc tcccccacgg 300

ggtgcgcgcc tggcccggcc cagccccctc tccggggttt ccccgggtgc tctcctcgct 360

ttctctttgt ctctgctgtt ctttctcggg ctcccgggtt cccacccgcc tgtgctctcc 420

ctctcgggcg tccgggccgg ttccctttaa ctttcttctt tcccggggtg aaaactttgc 480

tcggagctgg cggcagctcg cggacgttat tggccggcgc cccgcccggc ggccccgccc 540

cccgcccccg cgctcccctc cgcccctcac tcccagcgcg agtggcggcg gcggcggagc 600

cttcgggggc gagcgcgcgt gtgtgtgagt gcgcgccggc cagcgtgagt gtgtgtgcgc 660

cccgggcgcg ggcagggcag cactccgagc tcggcgggag cggcgggagc cgggcggccg 720

cgtagtcact cgggcgagag aggcggcggc ggggccggga ccggggctgg ggctggggca 780

gcggcggccg cgccgggcat ggagctggca agcccgcgct gaggcgggac gcgcctgcta 840

gcagcgagcg agaggctctc cggcgaccgg cgcgcgggct ccccggaggg gccaggcaaa 900

cttttctttc tcttttgccc cctccagagg taaagtcccg aacgcggact ttccggcggg 960

gacgcgatcg gggggcatct gagagggacc ccgggctgcg agacgaaggg gcgcgggccg 1020

tgcagagtcg gggtccccca gctctcctgc gcccgaaact tggggtgcga ggggggctgg 1080

tcgcggacgg ggagaccggc tcaggcatgc ccctcgggcg gcgtgggggc ggcggtggcg 1140

gggaagcaga gcgttctccc gccgggcggg gaagaagggg cgcgagcggt gcggacttgg 1200

agggccccgg cttcgccgcc cgcgggactt tgggggagag aggcgggcag tcggctgcgg 1260

ggtgggtgcc caggaagccg ggcgttctcc cgcatctccg ctcgccaccc cgccgagagc 1320

tggagggcgc ggggcgggct ggctgagcgc agctcccttc tctccgcagg cgccttctgc 1380

ggcaggcgga cagatcctcg gcgcggcagg gccggggcaa gctggacgca gcatgatgcg 1440

cgcagtgtgg gaggcgctgg cggcgctggc ggcggtggcg tgcctggtgg gcgcggtgcg 1500 cggcgggccc gggctcagca tgttcgcggg ccaggcggcg cagcccgatc cctgctcgga 1560

cgagaacggc cacccgcgcc gctgcatccc ggactttgtc aatgcggcct tcggcaagga 1620

cgtgcgcgtg tccagcacct gcggccggcc cccggcgcgc tactgcgtgg tgagcgagcg 1680

cggcgaggag cggctgcgct cgtgccacct ctgcaacgcg tccgacccca agaaggcgca 1740

cccgcccgcc ttcctcaccg acctcaacaa cccgcacaac ctgacgtgct ggcagtccga 1800

gaactacctg cagttcccgc acaacgtcac gctcacactg tccctcggca agaagttcga 1860

agtgacctac gtgagcctgc agttctgctc gccgcggccc gagtccatgg ccatctacaa 1920

gtccatggac tacgggcgca cgtgggtgcc cttccagttc tactccacgc agtgccgcaa 1980

gatgtacaac cggccgcacc gcgcgcccat caccaagcag aacgagcagg aggccgtgtg 2040

caccgactcg cacaccgaca tgcgcccgct ctcgggcggc ctcatcgcct tcagcacgct 2100

ggacgggcgg ccctcggcgc acgacttcga caactcgccc gtgctgcagg actgggtcac 2160

ggccacagac atccgcgtgg ccttcagccg cctgcacacg ttcggcgacg agaacgagga 2220

cgactcggag ctggcgcgcg actcgtactt ctacgcggtg tccgacctgc aggtgggcgg 2280

ccggtgcaag tgcaacggcc acgcggcccg ctgcgtgcgc gaccgcgacg acagcctggt 2340

gtgcgactgc aggcacaaca cggccggccc ggagtgcgac cgctgcaagc ccttccacta 2400

cgaccggccc tggcagcgcg ccacagcccg cgaagccaac gagtgcgtgg gtgagtgggg 2460

tgcggcggcg gagccggcgg cgggtggggc cgcgggcggg agctgctggg cctcgcagcg 2520

gcgagttcat aggagcgcgg gtcgagggaa cggcgggagg cgcgttcgcc gatgcccggg 2580

acccgggagg gctcagagca ggtccactcg ctcgcgtggc gctcgtggtg gacgcccgaa 2640

tttgcgccca gtgctctctg cgaagccaag aagcagcagg agaaatgttc ccgggagggg 2700

gtttggcaga acatttgcag ataggtctcc gctaaccctg gatccaaacg caaacattca 2760

ttgccttccc cctcgttggg ttggacgctg ggattcacct 2800

<210> SEQ ID NO 136
<211> LENGTH: 2800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 136

aggtgaatcc cagcgtccaa cccaacgagg gggaaggcaa tgaatgtttg cgtttggatc 60

cagggttagc ggagacctat ctgcaaatgt tctgccaaac cccctcccgg gaacatttct 120

cctgctgctt cttggcttcg cagagagcac tgggcgcaaa ttcgggcgtc caccacgagc 180

gccacgcgag cgagtggacc tgctctgagc cctcccgggt cccgggcatc ggcgaacgcg 240

cctcccgccg ttccctcgac ccgcgctcct atgaactcgc cgctgcgagg cccagcagct 300

cccgcccgcg gccccacccg ccgccggctc cgccgccgca ccccactcac ccacgcactc 360

gttggcttcg cgggctgtgg cgcgctgcca gggccggtcg tagtggaagg gcttgcagcg 420

gtcgcactcc gggccggccg tgttgtgcct gcagtcgcac accaggctgt cgtcgcggtc 480

gcgcacgcag cgggccgcgt ggccgttgca cttgcaccgg ccgcccacct gcaggtcgga 540

caccgcgtag aagtacgagt cgcgcgccag ctccgagtcg tcctcgttct cgtcgccgaa 600

cgtgtgcagg cggctgaagg ccacgcggat gtctgtggcc gtgacccagt cctgcagcac 660

gggcgagttg tcgaagtcgt gcgccgaggg ccgcccgtcc agcgtgctga aggcgatgag 720

gccgcccgag agcgggcgca tgtcggtgtg cgagtcggtg cacacggcct cctgctcgtt 780

ctgcttggtg atgggcgcgc ggtgcggccg gttgtacatc ttgcggcact gcgtggagta 840

-continued

gaactggaag ggcacccacg tgcgcccgta gtccatggac ttgtagatgg ccatggactc 900

gggccgcggc gagcagaact gcaggctcac gtaggtcact tcgaacttct tgccgaggga 960

cagtgtgagc gtgacgttgt gcgggaactg caggtagttc tcggactgcc agcacgtcag 1020

gttgtgcggg ttgttgaggt cggtgaggaa ggcgggcggg tgcgccttct tggggtcgga 1080

cgcgttgcag aggtggcacg agcgcagccg ctcctcgccg cgctcgctca ccacgcagta 1140

gcgcgccggg ggccggccgc aggtgctgga cacgcgcacg tccttgccga aggccgcatt 1200

gacaaagtcc gggatgcagc ggcgcgggtg gccgttctcg tccgagcagg gatcgggctg 1260

cgccgcctgg cccgcgaaca tgctgagccc gggcccgccg cgcaccgcgc ccaccaggca 1320

cgccaccgcc gccagcgccg ccagcgcctc ccacactgcg cgcatcatgc tgcgtccagc 1380

ttgccccggc cctgccgcgc cgaggatctg tccgcctgcc gcagaaggcg cctgcggaga 1440

gaagggagct gcgctcagcc agcccgcccc gcgccctcca gctctcggcg gggtggcgag 1500

cggagatgcg ggagaacgcc cggcttcctg ggcacccacc ccgcagccga ctgcccgcct 1560

ctctccccca aagtcccgcg ggcggcgaag ccggggccct ccaagtccgc accgctcgcg 1620

ccccttcttc cccgcccggc gggagaacgc tctgcttccc cgccaccgcc gcccccacgc 1680

cgcccgaggg gcatgcctga gccggtctcc ccgtccgcga ccagcccccc tcgcacccca 1740

agtttcgggc gcaggagagc tgggggaccc cgactctgca cggcccgcgc cccttcgtct 1800

cgcagcccgg ggtccctctc agatgccccc cgatcgcgtc cccgccggaa agtccgcgtt 1860

cgggacttta cctctggagg gggcaaaaga gaaagaaaag tttgcctggc ccctccgggg 1920

agcccgcgcg ccggtcgccg gagagcctct cgctcgctgc tagcaggcgc gtcccgcctc 1980

agcgcgggct tgccagctcc atgcccggcg cggccgccgc tgccccagcc ccagccccgg 2040

tcccggcccc gccgccgcct ctctcgcccg agtgactacg cggccgcccg gctcccgccg 2100

ctcccgccga gctcggagtg ctgccctgcc cgcgcccggg gcgcacacac actcacgctg 2160

gccggcgcgc actcacacac acgcgcgctc gcccccgaag gctccgccgc cgccgccact 2220

cgcgctggga gtgaggggcg gaggggagcg cgggggcggg gggcggggcc gccgggcggg 2280

gcgccggcca ataacgtccg cgagctgccg ccagctccga gcaaagtttt caccccggga 2340

aagaagaaag ttaaagggaa ccggcccgga cgcccgagag ggagagcaca ggcgggtggg 2400

aacccgggag cccgagaaag aacagcagag acaaagagaa agcgaggaga gcacccgggg 2460

aaaccccgga gagggggctg ggccgggcca ggcgcgcacc ccgtggggga ggagggggccg 2520

ccggggactg tcagcctcgc ccgcgccccg cgccgcccgg agagcctcac gcccggggga 2580

gcgcgcgggc gggggaaggg ggccactttc tccctcccgg tcccagccaa acacatctgt 2640

gtttgttttc tttgctgcgc ggaggtcggg ccttcctcta acccagcctg atggccccccg 2700

gtggcaccgc gcacagggct gtgcccctgt gggcacgcag cccgggagcg tgaggaagag 2760

gaggaggatg tgacctctgc ctgctctcca tttttgcccg 2800

<210> SEQ ID NO 137
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 137

gcagtcctgt gtgactggtg agactcttgt aggggcgttt ctacaacgac gaaacccttc 60

ctaggcactc actccaacag aataacaagc ccattttatt agtatttcgt tttccatgta 120

aagttctgct catacgaata tatttataat tctgattttt ttacggcatt ggggagcaca 180

-continued

```
ccgacaggct gctgaacggt ggctggagat tcgagggaaa acgaagttcg ccgaggcggc    240

ctcgggcggg caggtcccgg gctccatcac agggcacacg cggctaccag ggacgcagcc    300

ccccaacaca cacacacaca cacacacaca cacacacaca cacacacaca ccctctccca    360

ctcatgcctg gcaacccagc agaaacttcg gactggggca aaacaagccc gggccccggc    420

ggcacgcggg gctaggcgcg ttcccgccag tacctggtcg cgaggccgct cgcggggtgc    480

cctgcgtgcc ccccactccc gcagcccgcg ccctgctcgc tcactgtggg ggcgcagcgg    540

ccaggcttct ctgtttgttg tttaaagaaa tcctagggcg ggcgagcggc ggcatctagg    600

ggagggggcg cagccagaat tcccttccag caagcgcgtg aggggcattc tcaacgcaaa    660

accagaccca gaaagtagtg accagccctc ctcggattac ccttcattgg ctcctccctt    720

gctcccccca ccctccagat ttgcataaaa aaggccaaga aaactctggc tgtgccccag    780

caacggctca ttctgctccc ccgggtcgga gcccccccgga gctgcgcgcg ggcttgcagc    840

gcctcgcccg cgctgtcctc ccggtgtccc gcttctccgc gccccagccg ccggctgcca    900

gcttttcggg gccccgagtc gcacccagcg aagagagcgg gcccgggaca agctcgaact    960

ccggccgcct cgcccttccc cggctccgct ccctctgccc cctcggggtc gcgcgcccac   1020

gatgctgcag ggccctggct cgctgctgct gctcttcctc gcctcgcact gctgcctggg   1080

ctcggcgcgc gggctcttcc tctttggcca gcccgacttc tcctacaagc gcagcaattg   1140

caagcccatc cctgccaacc tgcagctgtg ccacggcatc gaataccaga acatgcggct   1200

gcccaacctg ctgggccacg agaccatgaa ggaggtgctg gagcaggccg gcgcttggat   1260

cccgctggtc atgaagcagt gccacccgga caccaagaag                         1300


<210> SEQ ID NO 138
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 138

cttcttggtg tccgggtggc actgcttcat gaccagcggg atccaagcgc cggcctgctc     60

cagcacctcc ttcatggtct cgtggcccag caggttgggc agccgcatgt tctggtattc    120

gatgccgtgg cacagctgca ggttggcagg gatgggcttg caattgctgc gcttgtagga    180

gaagtcgggc tggccaaaga ggaagagccc gcgcgccgag cccaggcagc agtgcgaggc    240

gaggaagagc agcagcagcg agccagggcc ctgcagcatc gtgggcgcgc gaccccgagg    300

gggcagaggg agcggagccg gggaagggcg aggcggccgg agttcgagct tgtcccgggc    360

ccgctctctt cgctgggtgc gactcggggc cccgaaaagc tggcagccgg cggctggggc    420

gcggagaagc gggacaccgg gaggacagcg cgggcgaggc gctgcaagcc cgcgcgcagc    480

tccgggggggc tccgacccgg gggagcagaa tgagccgttg ctggggcaca gccagagttt    540

tcttggcctt ttttatgcaa atctggaggg tgggggggagc aagggaggag ccaatgaagg    600

gtaatccgag gagggctggt cactactttc tgggtctggt tttgcgttga gaatgcccct    660

cacgcgcttg ctggaaggga attctggctg cgcccccctcc cctagatgcc gccgctcgcc    720

cgccctagga tttctttaaa caacaaacag agaagcctgg ccgctgcgcc cccacagtga    780

gcgagcaggg cgcgggctgc gggagtgggg ggcacgcagg gcaccccgcg agcggcctcg    840

cgaccaggta ctggcgggaa cgcgcctagc cccgcgtgcc gccggggccc gggcttgttt    900

tgccccagtc cgaagtttct gctgggttgc caggcatgag tgggagaggg tgtgtgtgtg    960

tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgttgggg ggctgcgtcc ctggtagccg   1020
```

cgtgtgccct gtgatggagc ccgggacctg cccgcccgag gccgcctcgg cgaacttcgt 1080

tttccctcga atctccagcc accgttcagc agcctgtcgg tgtgctcccc aatgccgtaa 1140

aaaaatcaga attataaata tattcgtatg agcagaactt tacatggaaa acgaaatact 1200

aataaaatgg gcttgttatt ctgttggagt gagtgcctag gaagggtttc gtcgttgtag 1260

aaacgcccct acaagagtct caccagtcac acaggactgc 1300

<210> SEQ ID NO 139
<211> LENGTH: 1034
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 139

gctgcctttg ttctttgact actcagccaa ttcaggtctg agctgttctt cgacgccgcc 60

ctagatgcga tgatgaaggt caggtgcccg catcccaccc accgtcccct cgcaggggcc 120

ctaggaccca cccagatccc gcctgtctct ctccccgcgg caggttccgc tgcatcgtgc 180

accctttccg cgagaagctg accctgcgga aggcgctcgt caccatcgcc gtcatctggg 240

ccctggcgct gctcatcatg tgtccctcgg ccgtcacgct gaccgtcacc cgtgaggagc 300

accacttcat ggtggacgcc cgcaaccgct cctacccgct ctactcctgc tgggaggcct 360

ggcccgagaa gggcatgcgc agggtctaca ccactgtgct cttctcgcac atctacctgg 420

cgccgctggc gctcatcgtg gtcatgtacg cccgcatcgc gcgcaagctc tgccaggccc 480

cgggcccggc cccgggggc gaggaggctg cggacccgcg agcatcgcgg cgcagagcgc 540

gcgtggtgca catgctggtc atggtggcgc tgttcttcac gctgtcctgg ctgccgctct 600

gggcgctgct gctgctcatc gactacgggc agctcagcgc gccgcagctg cacctggtca 660

ccgtctacgc cttccccttc gcgcactggc tggccttctt caacagcagc gccaacccca 720

tcatctacgg ctacttcaac gagaacttcc gccgcggctt ccaggccgcc ttccgcgccc 780

gcctctgccc gcgcccgtcg gggagccaca aggaggccta ctccgagcgg cccggcgggc 840

ttctgcacag gcgggtcttc gtggtggtgc ggcccagcga ctccgggctg ccctctgagt 900

cgggccctag cagtggggcc cccaggcccg gccgcctccc gctgcggaat gggcgggtgg 960

ctcaccacgg cttgcccagg gaagggcctg gctgctccca cctgcccctc accattccag 1020

cctgggatat ctga 1034

<210> SEQ ID NO 140
<211> LENGTH: 1034
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 140

tcagatatcc caggctggaa tggtgagggg caggtgggag cagccaggcc cttccctggg 60

caagccgtgg tgagccaccc gcccattccg cagcgggagg cggccgggcc tgggggcccc 120

actgctaggg cccgactcag agggcagccc ggagtcgctg ggccgcacca ccacgaagac 180

ccgcctgtgc agaagcccgc cgggccgctc ggagtaggcc tccttgtggc tccccgacgg 240

gcgcgggcag aggcgggcgc ggaaggcggc ctggaagccg cggcggaagt tctcgttgaa 300

gtagccgtag atgatggggt tggcgctgct gttgaagaag gccagccagt gcgcgaaggg 360

gaaggcgtag acggtgacca ggtgcagctg cggcgcgctg agctgcccgt agtcgatgag 420

cagcagcagc gcccagagcg gcagccagga cagcgtgaag aacagcgcca ccatgaccag 480

catgtgcacc acgcgcgctc tgcgccgcga tgctcgcggg tccgcagcct cctcgccccc 540 gggggccggg cccggggcct ggcagagctt gcgcgcgatg cgggcgtaca tgaccacgat 600

gagcgccagc ggcgccaggt agatgtgcga gaagagcaca gtggtgtaga ccctgcgcat 660

gcccttctcg ggccaggcct cccagcagga gtagagcggg taggagcggt tgcgggcgtc 720

caccatgaag tggtgctcct cacgggtgac ggtcagcgtg acggccgagg gacacatgat 780

gagcagcgcc agggcccaga tgacggcgat ggtgacgagc gccttccgca gggtcagctt 840

ctcgcggaaa gggtgcacga tgcagcggaa cctgccgcgg ggagagagac aggcgggatc 900

tgggtgggtc ctagggcccc tgcgagggga cggtgggtgg gatgcgggca cctgaccttc 960

atcatcgcat ctagggcggc gtcgaagaac agctcagacc tgaattggct gagtagtcaa 1020

agaacaaagg cagc 1034

<210> SEQ ID NO 141
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 141

agaaaggtaa tatttggagg cctccgaggg acgggcaggg gaaagaggga tcctctgacc 60

cagcgggggc tgggaggatg gctgtttttg tttttccca cctagcctcg gaatcgcgga 120

ctgcgcccag tgacggactc aaacttaccc ttccctctga ccccgccgta ggatgacgcc 180

tcaaccctcg ggtgcgccca ctgtccaagt gacccgtgag acggagcggt ccttccccag 240

agcctcggaa gacgaagtga cctgccccac gtccgccccg cccagcccca ctcgcacacg 300

ggggaactgc gcagaggcgg aagagggagg ctgccgaggg gccccgagga agctccgggc 360

acggcgcggg ggacgcagcc ggcctaagag cgagttggca ctgagcaagc agcgacggag 420

tcggcgaaag aaggccaacg accgcgagcg caatcgaatg cacaacctca actcggcact 480

ggacgccctg cgcggtgtcc tgcccacctt cccagacgac gcgaagctca ccaagatcga 540

gacgctgcgc ttcgcccaca actacatctg ggcgctgact caaacgctgc gcatagcgga 600

ccacagcttg tacgcgctgg agccgccggc gccgcactgc ggggagctgg gcagcccagg 660

cggttccccc ggggactggg ggtccctcta ctccccagtc tcccaggctg gcagcctgag 720

tcccgccgcg tcgctggagg agcgacccgg gctgctgggg gccacctttt ccgcctgctt 780

gagcccaggc agtctggctt 800

<210> SEQ ID NO 142
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 142

aagccagact gcctgggctc aagcaggcgg aaaaggtggc ccccagcagc ccgggtcgct 60

cctccagcga cgcggcggga ctcaggctgc cagcctggga gactggggag tagagggacc 120

cccagtcccc gggggaaccg cctgggctgc ccagctcccc gcagtgcggc gccggcggct 180

ccagcgcgta caagctgtgg tccgctatgc gcagcgtttg agtcagcgcc cagatgtagt 240

tgtgggcgaa gcgcagcgtc tcgatcttgg tgagcttcgc gtcgtctggg aaggtgggca 300

ggacaccgcg cagggcgtcc agtgccgagt tgaggttgtg cattcgattg cgctcgcggt 360

cgttggcctt ctttcgccga ctccgtcgct gcttgctcag tgccaactcg ctcttaggcc 420

ggctgcgtcc cccgcgccgt gcccggagct tcctcggggc ccctcggcag cctccctctt 480

ccgcctctgc gcagttcccc cgtgtgcgag tggggctggg cggggcggac gtggggcagg 540

-continued

tcacttcgtc ttccgaggct ctggggaagg accgctccgt ctcacgggtc acttggacag 600

tgggcgcacc cgagggttga ggcgtcatcc tacggcgggg tcagagggaa gggtaagttt 660

gagtccgtca ctgggcgcag tccgcgattc cgaggctagg tgggaaaaaa caaaaacagc 720

catcctccca gcccccgctg ggtcagagga tccctctttc ccctgcccgt ccctcggagg 780

cctccaaata ttacctttct 800

<210> SEQ ID NO 143
<211> LENGTH: 1550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 143

taaagcttcc ccagagggag gaaaggtggg ggcggggcgg ctgctgaggc ccaggatata 60

agggctggag gtgctgcttt caggcctggc cagcccacca tgcacgccca ctgcctgccc 120

ttccttctgc acgcctggtg ggccctactc caggcgggtg ctgcgacggt ggccactgcg 180

ctcctgcgta cgcgggggca gccctcgtcg ccatcccctc tggcgtacat gctgagcctc 240

taccgcgacc cgctgccgag ggcagacatc atccgcagcc tacaggcaga aggtaggcag 300

tgccgcgtgc cgcgccctgc tgggcacccc cggggcgcct ccgccgcgtc cagccagcgg 360

actcgggaag tgctgtgggt tgggggctgc ggctccgagc cgggtttgca gccgcccggg 420

cgtcccgagc ccagggccta gctctgcggg tgtctccgcg tcagcaggct cggggtgcag 480

cgttggtggc tgggggcgta tccacggccg agtcgggaag ggattctagc gttcagggtg 540

tgtcctcgac ggggaccatt gtctctgggt tttggtttgg gattgcgcgg agcgcagcgc 600

ggaagggtgg gagcttctaa tctccagtct tgtgaagttg cttatcccgg agcctgggtc 660

tgcgcatctg taggataggt gtaataaata acacctcgcc tatcagactg tggaaagcgc 720

gagatgacaa tgcgcgcgaa acgctcagcg cagtacccgg cacagccaca gtcaacggtc 780

gttggtatta ctgtaatggt ttggtcttgg cgattttttt ttctttctgc gagtgagggt 840

gaatgggtcc cggggtgtga cgtcgggagt atcggcagct gagctggtaa catcggggat 900

tcgggctcac ggcccggaga tcagggatgg gctgtcccga agtcgcgaac tgtggcagcc 960

ttgggtcctc cagccgcgcc ggggaagtgt caagtgtctc gcttaacccc gggttcgggg 1020

ccatgatttg caggggagtg ggtgtcaagg acggcaggga tctgagggta tcgccctcga 1080

ggacctggca gcgcgttctg ggcacccagc gcggcgagca ggtgggtgct gcggagaggg 1140

agccccttcc gcgcctcaat ccacattctg ccgcctgggc agccgcggcc gcccacgcct 1200

ccctccgcct gcgggggcca gacggccctc cctggggccg gggcgcaatc cacaaacgct 1260

aatctgatcc gacctgccgc ctgcccgccc cttgtgacct ggtgccgggg gcccttcgct 1320

cccgcgcctg ggtcagacag gccggtgacc ctctccggaa gggtcatctg ggaccagcc 1380

agaccagggg acaccctcgg gggcggggca atgagaaatt tgctggagtg ctcggcccct 1440

caaccgaaaa gcggccgggg atgggagggg gcaaagaagg gagggagcgc ttttccagtt 1500

cactcccttc tggaaagttc gagatgtgtg cggtgatgga caggcatctg 1550

<210> SEQ ID NO 144
<211> LENGTH: 1550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 144

cagatgcctg tccatcaccg cacacatctc gaactttcca gaagggagtg aactggaaaa 60

-continued

gcgctccctc ccttctttgc cccctcccat ccccggccgc ttttcggttg aggggccgag 120

cactccagca aatttctcat tgccccgccc ccgagggtgt cccctggtct ggctggtccc 180

cagatgaccc ttccggagag ggtcaccggc tgtctgaccc caggcgcggg agcgaagggc 240

ccccggcacc aggtcacaag gggcgggcag gcggcaggtc ggatcagatt agcgtttgtg 300

gattgcgccc cggccccagg gagggccgtc tggcccccgc aggcggaggg aggcgtgggc 360

ggccgcggct gcccaggcgg cagaatgtgg attgaggcgc ggaaggggct ccctctccgc 420

agcacccacc tgctcgccgc gctgggtgcc cagaacgcgc tgccaggtcc tcgagggcga 480

taccctcaga tccctgccgt ccttgacacc cactcccctg caaatcatgg ccccgaaccc 540

ggggttaagc gagacacttg acacttcccc ggcgcggctg gaggacccaa ggctgccaca 600

gttcgcgact tcgggacagc ccatccctga tctccgggcc gtgagcccga atccccgatg 660

ttaccagctc agctgccgat actcccgacg tcacaccccg ggacccattc accctcactc 720

gcagaaagaa aaaaaaatcg ccaagaccaa accattacag taataccaac gaccgttgac 780

tgtggctgtg ccgggtactg cgctgagcgt ttcgcgcgca ttgtcatctc gcgctttcca 840

cagtctgata ggcgaggtgt tatttattac acctatccta cagatgcgca gacccaggct 900

ccgggataag caacttcaca agactggaga ttagaagctc ccacccttcc gcgctgcgct 960

ccgcgcaatc ccaaaccaaa acccagagac aatggtcccc gtcgaggaca caccctgaac 1020

gctagaatcc cttcccgact cggccgtgga tacgccccca gccaccaacg ctgcaccccg 1080

agcctgctga cgcggagaca cccgcagagc taggccctgg gctcgggacg cccgggcggc 1140

tgcaaacccg gctcggagcc gcagccccca acccacagca cttcccgagt ccgctggctg 1200

gacgcggcgg aggcgccccg ggggtgccca gcagggcgcg gcacgcggca ctgcctacct 1260

tctgcctgta ggctgcggat gatgtctgcc ctcggcagcg ggtcgcggta gaggctcagc 1320

atgtacgcca gaggggatgg cgacgagggc tgcccccgcg tacgcaggag cgcagtggcc 1380

accgtcgcag cacccgcctg gagtagggcc caccaggcgt gcagaaggaa gggcaggcag 1440

tgggcgtgca tggtgggctg gccaggcctg aaagcagcac ctccagccct tatatcctgg 1500

gcctcagcag ccgccccgcc cccacctttc ctccctctgg ggaagcttta 1550

<210> SEQ ID NO 145
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 145

accccggggc gtgggagaag cccctgcttg gggggaccgt ctgctgttta ggggctcccc 60

ttcgacacgt gggaggcaaa agtgcagagc gcaccatcat ccagctccgg ccgcactgca 120

cagcgaggcc ggcccggagc ccggatgctg ggctcggtcc cgccgaggct cggcctggct 180

gtaaagcaga ggggggcgag ggaagccggg ccagcgggtg tcgcgggtag ccggcgtccg 240

ggacggggtg tggcgcccag agcgctgctg cctctcgcag ccaggaggct ggatgtcggg 300

tttgggtgtc ttccagaagg agccgcacta gcgacgaggg aagaggaact ggcttcccgg 360

gcagtctccc ccgccccaaa cttttcctcc tcgcggaggg tgggcgggcg gagggaggaa 420

gcgcagccgg ggaacgtggc gcccgcgttc ctcccgcccg ggggctgcgg ctgggctgag 480

tgtgtcttta aatctgagcc ccccgcccct cgcggtgggg ccgggactcg cggtccgggc 540

gggggcgggc gcggtgattg gcggccgggt cgggtccgcc cctcggcgtt gggtagcggg 600

gcgctgggga gcagcgcggc gcgcacgggc cggggcgcgc aggtcccgtc gccggtgagc 660 acgggctccc tctcgcgtgg cctcgccggg tccgcctggc ctgcccacct ccggagccac 720

ctctgccccc gcatgggctg gcgaagttgg gaggagcgag ctggagccag agcgcgcgcc 780

gggcgcgccc cgtcgctgcc tgactcggcg cccgcagttc gggcgcagca cgccggccgc 840

aggagcacgg atgccccccg gagccgcggg ctggcaggta ccgaagtgtc ctgccctggg 900

gctggcgagg ggagggcaaa tctggaatcc cccgggcacc ccccagcccg aggctgctcc 960

agacaccaac tccccatcct ttggagaggt gaggtcctgg gccttcaccc cacacccgct 1020

caggattggt ccctgggagg caagagggac 1050

<210> SEQ ID NO 146
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 146

gtccctcttg cctcccaggg accaatcctg agcgggtgtg gggtgaaggc ccaggacctc 60

acctctccaa aggatgggga gttggtgtct ggagcagcct cgggctgggg ggtgcccggg 120

ggattccaga tttgccctcc cctcgccagc cccagggcag gacacttcgg tacctgccag 180

cccgcggctc cggggggcat ccgtgctcct gcggccggcg tgctgcgccc gaactgcggg 240

cgccgagtca ggcagcgacg gggcgcgccc ggcgcgcgct ctggctccag ctcgctcctc 300

ccaacttcgc cagcccatgc gggggcagag gtggctccgg aggtgggcag gccaggcgga 360

cccggcgagg ccacgcgaga gggagcccgt gctcaccggc gacgggacct gcgcgccccg 420

gcccgtgcgc gccgcgctgc tccccagcgc cccgctaccc aacgccgagg ggcggacccg 480

acccggccgc caatcaccgc gcccgccccc gcccggaccg cgagtcccgg ccccaccgcg 540

aggggcgggg ggctcagatt taaagacaca ctcagcccag ccgcagcccc cgggcgggag 600

gaacgcgggc gccacgttcc ccggctgcgc ttcctccctc cgcccgccca ccctccgcga 660

ggaggaaaag tttggggcgg gggagactgc ccgggaagcc agttcctctt ccctcgtcgc 720

tagtgcggct ccttctggaa gacacccaaa cccgacatcc agcctcctgg ctgcgagagg 780

cagcagcgct ctgggcgcca caccccgtcc cggacgccgg ctacccgcga cacccgctgg 840

cccggcttcc ctcgcccccc tctgctttac agccaggccg agcctcggcg ggaccgagcc 900

cagcatccgg gctccgggcc ggcctcgctg tgcagtgcgg ccggagctgg atgatggtgc 960

gctctgcact tttgcctccc acgtgtcgaa ggggagcccc taaacagcag acggtccccc 1020

caagcagggg cttctcccac gccccggggt 1050

<210> SEQ ID NO 147
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 147

ccgaaaggac ccgtcccagc gagccagggc ctggttttcc ttccgcagaa ggcggaggga 60

ccggagcggg cgcgggcacc cctgggctct gaggggcgcg ctctgaaggg cggcggactt 120

cagggccatg ctggctgtcc ccagaaagca ggagcccgaa accgcggggc caacgaacgc 180

ccacattctc tgctacaacc tcgccactcc cctgcgcctc tccccttgcc ccctgccccc 240

acaggtaacg cccagaacga gtgcttctcc cggtggggta ctgaggagcc tgggctgcag 300

ctgccgagcc gccacagcca cgctgagccc ggcctggcct gcacactggc gccaccgcct 360

ggcggggagc gggactgacg cgctcctctc cctctcctcc agcccagatc acggaggcgc 420

-continued

ggagctccat ctcctgccct gggcgagggg agtgagggag acaaagactt tgggcacaac 480

acccaccaca tagaacctat tctctagttg ggaaacaagt caaggcaaag gcgcacagag 540

tgaaagtcag 550

<210> SEQ ID NO 148
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 148

ctgactttca ctctgtgcgc ctttgccttg acttgtttcc caactagaga ataggttcta 60

tgtggtgggt gttgtgccca aagtctttgt ctccctcact cccctcgccc agggcaggag 120

atggagctcc gcgcctccgt gatctgggct ggaggagagg gagaggagcg cgtcagtccc 180

gctccccgcc aggcggtggc gccagtgtgc aggccaggcc gggctcagcg tggctgtggc 240

ggctcggcag ctgcagccca ggctcctcag taccccaccg ggagaagcac tcgttctggg 300

cgttacctgt gggggcaggg ggcaagggga gaggcgcagg ggagtggcga ggttgtagca 360

gagaatgtgg gcgttcgttg gccccgcggt ttcgggctcc tgctttctgg ggacagccag 420

catggccctg aagtccgccg cccttcagag cgcgcccctc agagcccagg ggtgcccgcg 480

cccgctccgg tccctccgcc ttctgcggaa ggaaaaccag gccctggctc gctgggacgg 540

gtcctttcgg 550

<210> SEQ ID NO 149
<211> LENGTH: 1550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 149

ccctccagtt tgctggagtt gccggattac attgttcctc cccggtgtgc ggcgtgagct 60

tcccccaccc gagcgcccaa caagtctcct ttctccagcc tgcgcgctgc tgcgctgagg 120

ccgaatgaag cgcagcacgg tgcgggcagc ccgaggcccc gaggctgggc tctgtctgtc 180

tgggactgcg ccgtgcccag cctcggtccc ctctctgtgg gtaaggatgg ttgagtccag 240

cctccacggc agcggctcct tgtgccacta gcagcccttc ttctgcgctc tccgcctttt 300

ctctctagac tggatctctc ctcccccccg cgccccccctc cccgcatctc ccactcgctg 360

gctctctctc cagctgcctc ctctccaggt ctctcctggc tgcgcgcgct cctctccccg 420

cttctccccc tcccgcagcc tcgccgcctt ggtgccttcc tgcccggctc ggccggcgct 480

cgtccccggc cccggccccg ccagcccggg tctccgcgct cggagcagct cagccctgca 540

gtggctcggg acccgatgct atgagaggga agcgagccgg gcgcccagac cttcaggagg 600

cgtcggatgc gcggcgggtc ttgggaccgg gctctctctc cggctcgcct tgccctcggg 660

tgattatttg gctccgctca tagccctgcc ttcctcggag gagccatcgg tgtcgcgtgc 720

gtgtggagta tctgcagaca tgactgcgtg gaggagattc cagtcgctgc tcctgcttct 780

cgggctgctg gtgctgtgcg cgaggctcct cactgcagcg aagggtaaga cggacttgct 840

cctggccggg gaggcggtag agccctcgga ggccccgtgt gcggacgcga gtgtgcgttt 900

tggggaccgc agggtacgga gtggccgcct ctgcccggcg ctgctccatc gccgaagctc 960

ggggaacgcg atgcacggga gggagcttcc atcgcgctct ccccagccct cctgggcccc 1020

cgccccaccc cgccattcct tccccctctc ttgggctcac aggagagatc tctttttctc 1080

ggcagtacag ggtgtcaagg agaaaggaac ccaatacgag ttgggctgga actgtgctcc 1140 gccggggcgg tgttgcctcc tccgagacgt ggactccacg ggtcggggtg gctgaggggc 1200

agttcccagg actttctccc cggacccgac gcgcctggga aagcgtcccg ggtgaagccg 1260

gcctggaaag ttcgggctct ctacgggggt tttggtacca ataggcaaag gtctccgccg 1320

gcccggcctc ctcgcaccca tacaccccat tcctcctctc ctccttccct ctccaacgtc 1380

ctcagccggc gaggagtagc tgcctctaga aggtcgcccc cgctttcctc tcccccggac 1440

ttcgctcctt gcaagttgta aggtgttggc aaggtgcgtg aaacaggcta ggagttctgg 1500

accggcttcc aagtcagata cattcactgt gggcgcacgg gtatcctcct 1550

<210> SEQ ID NO 150
<211> LENGTH: 1550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 150

aggaggatac ccgtgcgccc acagtgaatg tatctgactt ggaagccggt ccagaactcc 60

tagcctgttt cacgcacctt gccaacacct tacaacttgc aaggagcgaa gtccggggga 120

gaggaaagcg ggggcgacct tctagaggca gctactcctc gccggctgag gacgttggag 180

agggaaggag gagaggagga atggggtgta tgggtgcgag gaggccgggc cggcggagac 240

ctttgcctat tggtaccaaa acccccgtag agagcccgaa ctttccaggc cggcttcacc 300

cgggacgctt tcccaggcgc gtcgggtccg gggagaaagt cctgggaact gcccctcagc 360

caccccgacc cgtggagtcc acgtctcgga ggaggcaaca ccgccccggc ggagcacagt 420

tccagcccaa ctcgtattgg gttcctttct ccttgacacc ctgtactgcc gagaaaaaga 480

gatctctcct gtgagcccaa gagaggggga aggaatggcg gggtggggcg ggggcccagg 540

agggctgggg agagcgcgat ggaagctccc tcccgtgcat cgcgttcccc gagcttcggc 600

gatggagcag cgccgggcag aggcggccac tccgtaccct gcggtcccca aaacgcacac 660

tcgcgtccgc acacggggcc tccgagggct ctaccgcctc cccggccagg agcaagtccg 720

tcttaccctt cgctgcagtg aggagcctcg cgcacagcac cagcagcccg agaagcagga 780

gcagcgactg gaatctcctc cacgcagtca tgtctgcaga tactccacac gcacgcgaca 840

ccgatggctc ctccgaggaa ggcagggcta tgagcggagc caaataatca cccgagggca 900

aggcgagccg gagagagagc ccggtcccaa gacccgccgc gcatccgacg cctcctgaag 960

gtctgggcgc ccggctcgct tccctctcat agcatcgggt cccgagccac tgcagggctg 1020

agctgctccg agcgcggaga cccgggctgg cggggccggg gccggggacg agcgccggcc 1080

gagccgggca ggaaggcacc aaggcggcga ggctgcggga gggggagaag cggggagagg 1140

agcgcgcgca gccaggagag acctggagag gaggcagctg gagagagagc cagcgagtgg 1200

gagatgcggg gagggggcg cgggggggag gagagatcca gtctagagag aaaaggcgga 1260

gagcgcagaa gaagggctgc tagtggcaca aggagccgct gccgtggagg ctggactcaa 1320

ccatccttac ccacagagag gggaccgagg ctgggcacgg cgcagtccca gacagacaga 1380

gcccagcctc ggggcctcgg gctgcccgca ccgtgctgcg cttcattcgg cctcagcgca 1440

gcagcgcgca ggctggagaa aggagacttg ttgggcgctc gggtggggga agctcacgcc 1500

gcacaccggg gaggaacaat gtaatccggc aactccagca aactggaggg 1550

<210> SEQ ID NO 151
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

```
<400> SEQUENCE: 151

tcctccttga gcagggagac catcggggtg caacctggcc ggggcgggga ggaggtgcag     60

ggcattgcca gagcgggcct gtccatgggc aagggacagc gacctcctgg gccaggacat    120

gtgagagctg cgcaggcctg ggcccggcgt ggcggaggtg cgcgagagcg gccagaagag    180

ggcgccagag agccaggcgc ggcccgcgga ggagcccgcg ccggccccta tacccagctc    240

cgcgccgcgc ggacccaccg agcccgcgct cagacgcccc agctccaccg agaggccgct    300

cgggccgtgt ccttcctctt ctccaggtgc aggcagagcc cccgagccat ggccagccct    360

tccggcagct ccgaagccac tggcaagccc cgaggcaggg atggccggcc caggagggag    420

gaggacgacg tccctcccga agagaagagg ctggggctgt agctggaggg gggaagcgca    480

cagcccgagg actgcgagaa cggggaggac gcgccgcggc caggcaggga ggagaccggc    540

acccagacag gtggcgaccg cagaggagta agtgacgcgg gcgctggggt ccgggggtgc    600

cgggggcgcc ggtaggggcg gcgggaggct ccgtggccgg ccccgggttg aagttggtat    660

tttagcggca actccgaagg gcgcggagtg acagcgcgtg acggcctccg agacgccagc    720

tgccgcttct cggctgtgtg gctttgactt cctgattctc ccacgacgtc gctggctggg    780

agacccactg gactctgcgg ctggccaaaa agagaggggc agccccgcgt cctgggggcc    840

cctagcaggg gaagtggcgg gtgttgcgct gggcatcctg tctggggcat ctgtctggga    900

ccctgttggt gcctctcacc tggcgagggg ccagtggtgg gggtaggggg gaagtccctg    960

gcgccaggct tggccaagcc ctgcttggct ggactgcggg ctggcggcgc tcacccagct   1020

cctcacctgt cccgcatctt cctgtttttc                                   1050


<210> SEQ ID NO 152
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 152

gaaaaacagg aagatgcggg acaggtgagg agctgggtga gcgccgccag cccgcagtcc     60

agccaagcag ggcttggcca agcctggcgc cagggacttc ccccctaccc ccaccactgg    120

cccctcgcca ggtgagaggc accaacaggg tcccagacag atgccccaga caggatgccc    180

agcgcaacac ccgccacttc ccctgctagg ggcccccagg acgcggggct gcccctctct    240

ttttggccag ccgcagagtc cagtgggtct cccagccagc gacgtcgtgg gagaatcagg    300

aagtcaaagc cacacagccg agaagcggca gctggcgtct cggaggccgt cacgcgctgt    360

cactccgcgc ccttcggagt tgccgctaaa ataccaactt caacccgggg ccggccacgg    420

agcctcccgc cgcccctacc ggcgcccccg gcacccccgg accccagcgc ccgcgtcact    480

tactcctctg cggtcgccac ctgtctgggt gccggtctcc tccctgcctg gccgcggcgc    540

gtcctccccg ttctcgcagt cctcgggctg tgcgcttccc ccctccagct acagccccag    600

cctcttctct tcgggaggga cgtcgtcctc ctccctcctg ggccggccat ccctgcctcg    660

gggcttgcca gtggcttcgg agctgccgga agggctggcc atggctcggg ggctctgcct    720

gcacctggag aagaggaagg acacggcccg agcggcctct cggtggagct ggggcgtctg    780

agcgcgggct cggtgggtcc gcgcggcgcg gagctgggta taggggccgg cgcgggctcc    840

tccgcgggcc gcgcctggct ctctggcgcc ctcttctggc cgctctcgcg cacctccgcc    900

acgccgggcc caggcctgcg cagctctcac atgtcctggc ccaggaggtc gctgtccctt    960

gcccatggac aggcccgctc tggcaatgcc ctgcacctcc tccccgcccc ggccaggttg   1020
```

caccccgatg gtctccctgc tcaaggagga 1050

<210> SEQ ID NO 153
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 153

cccagtaagt caccaattaa gtctttacta cttaaaagca aaatccacct atgtcctgaa 60

cagtatccac tttacgagcc tcattatatg tacgagataa aattcagaaa taaataaata 120

tacatgtata cgtatacaaa tatatttcaa attaaaaaat acttttagat agtggtatgt 180

attacattta gaaattaata acgaagtaaa ttatgggatg tcatccacgc ctgtcccaaa 240

ggtaccgaat ttataaatca tctcaggtgc ggagcaggac aggttgaaaa taggaatgac 300

atgaacccgc gcggaacagc tgccggcgcg gtgtccaggg cggcaccccg cccggtcccg 360

gcccctccag ccctgggccc gacccctact acgcctctgc ctcgacgcga acgcggagcc 420

cgagcgcgcg tcacgccgtg tggggccgaa gaggctgcta cccagaggcg gagtgcgggc 480

tcgcgagggt ccccacccga ctctcgctcc cgccagcacc tacggactcg cgtccccgcc 540

gcgcgccgac tcgggagcag caccgccccc ggcacaggag cctcacgcgc ctcttaccta 600

acaggaagtt gggtggaagc agcgcggacc cacggcacac cgaacgcact ccaacagaac 660

ccgacgcaga cacgcgcttt caaccggcgg agacactggc agggccagaa acgcgcgcag 720

cgggggcggg aggtcggtaa gctccccgcc cctgcccgag accccgcccc ggcccggccc 780

cgccttttc tctgcctccc ctccctgcac gtacgggccc cgcccctcgc gcgacgtttt 840

ttgttgaccc ggaaacggat tctccggagc cgaggtccgc tcgggtgagt gccctccgct 900

ttttgtggcc aaacccagcc acgcagttcc cttcctgcgg cgtcctccac acccggggtc 960

tgctggtctc cgcggatgtc acaggctcgg caaccgccct cctgtcggcg gggagtcccg 1020

cgacgcccgg aaatgctccg aagcctgtcg cccagctgcc agatctgcgt ctgtgtccgg 1080

ttccgtcact gaggtcgccc ctgtccggcc cttccaccct agttctcttc accgtccgcc 1140

catcctatcg cgcgcggcct caggtcccga ttcggcatgt ggcttgtctt ccatcgtccc 1200

caccctcgcc cctcttggcc cctcagggca gccctgggat tcggcagacg ccagtcctcc 1260

ctgagatgct tccccatcct tccctccgcc aggccctacg 1300

<210> SEQ ID NO 154
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 154

cgtagggcct ggcggaggga aggatgggga agcatctcag ggaggactgg cgtctgccga 60

atcccagggc tgccctgagg ggccaagagg ggcgagggtg gggacgatgg aagacaagcc 120

acatgccgaa tcgggacctg aggccgcgcg cgataggatg ggcggacggt gaagagaact 180

agggtggaag ggccggacag gggcgacctc agtgacggaa ccggacacag acgcagatct 240

ggcagctggg cgacaggctt cggagcattt ccgggcgtcg cgggactccc cgccgacagg 300

agggcggttg ccgagcctgt gacatccgcg gagaccagca gaccccgggt gtggaggacg 360

ccgcaggaag ggaactgcgt ggctgggttt ggccacaaaa agcggagggc actcacccga 420

gcggacctcg gctccggaga atccgtttcc gggtcaacaa aaaacgtcgc gcgagggggcg 480

gggcccgtac gtgcagggag gggaggcaga gaaaaaggcg gggccgggcc ggggcggggt 540

-continued

ctcgggcagg ggcggggagc ttaccgacct cccgcccccg ctgcgcgcgt ttctggccct 600

gccagtgtct ccgccggttg aaagcgcgtg tctgcgtcgg gttctgttgg agtgcgttcg 660

gtgtgccgtg ggtccgcgct gcttccaccc aacttcctgt taggtaagag gcgcgtgagg 720

ctcctgtgcc gggggcggtg ctgctcccga gtcggcgcgc ggcggggacg cgagtccgta 780

ggtgctggcg ggagcgagag tcgggtgggg accctcgcga gcccgcactc cgcctctggg 840

tagcagcctc ttcggcccca cacggcgtga cgcgcgctcg ggctccgcgt tcgcgtcgag 900

gcagaggcgt agtaggggtc gggcccaggg ctggaggggc cgggaccggg cggggtgccg 960

ccctggacac cgcgccggca gctgttccgc gcgggttcat gtcattccta ttttcaacct 1020

gtcctgctcc gcacctgaga tgatttataa attcggtacc tttgggacag gcgtggatga 1080

catcccataa tttacttcgt tattaatttc taaatgtaat acataccact atctaaaagt 1140

atttttaat ttgaaatata tttgtatacg tatacatgta tatttattta tttctgaatt 1200

ttatctcgta catataatga ggctcgtaaa gtggatactg ttcaggacat aggtggattt 1260

tgcttttaag tagtaaagac ttaattggtg acttactggg 1300

<210> SEQ ID NO 155
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 155

accggcgtcc cgctgggggc gcgcgagccc cacccccaga gatgctgact cagcaagtcg 60

ggaggggttg gggtgggac ctgccaatct gcatttccaa ccggcgccca ggtgacgctg 120

actctgctgg tctaccgtct tgggggtcac ctaattttc agcgatgcct cccagctggg 180

gaggccaaga agtgcctcgc tcaaggtctt ccaacacccg acctccagac cctcaatcct 240

gggccagcta caccgcaaac ctttccagct gtctctcctg cgccctgcgt ttcttcccca 300

cgtcacttgc cagggagccg ctaaacagca agaccgcgcg ctctgcggct ccagagtgcg 360

gatttcggtc gcgtgcggct ctgaccgcgt cgccccatcc ctggcggggc cacgcacgga 420

cgccatggct ggcgccgcgg agccgggcga tgcgcgcgga ctctcccggg gccctgactg 480

tccctgagtc ctccctgcgg ggggcgtgcg cggcccgccc cccgcggcgc cacgcggccc 540

ctcctcggcc ggggattggt gcgccgggcg gggcggggcg gggcgggata aaggcgcggg 600

gtctggctgc gcggggtctg cgggcagctc caactctggg ttcgtagttt gcgctgggtg 660

cgcaggaagg tcagtgtggg ggtcgcccga catttccccc ccgcggaggt gggagccgag 720

ccacatcttg gagtggggac tggccgcgga gcgggttgcc cagggccggc cgaggtcggg 780

gcgagccctg cgcggcgctg gagactctgc attcccgggc gcgcgcaggg tccccggccg 840

tggtcgcaga gtcaggaggg gcggctccgg agcccggcgc ggggagggcc caggcgcagt 900

cggggttggc agggcgcgac actcgctccc ctccactttt gaaagggctt cccacgccga 960

gaagaggggc gggcatggcc ggcccggcga aaccggtttg tacagacttt gggaagccat 1020

cgcctgcgga gggtgggacc ccacagcttg tccacctgcc caggctgaga cctcgtgtcc 1080

tagtcctgga tgccccacgg gtttctcgtc ccgggcagcg gcgcacggga ggagaagact 1140

cccggtctgc agtcagacct ccctctgaga ccctccctag ctcaggctta gagctttggg 1200

atttttctcg atcctttcta gctttcagat catccccacg taaagttcag actttaccag 1260

cccagagagt ttaaaaaaaa aaaaagagag agagagaaag 1300

<210> SEQ ID NO 156

<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 156

ctttctctct ctctcttttt ttttttttaa actctctggg ctggtaaagt ctgaacttta 60

cgtggggatg atctgaaagc tagaaaggat cgagaaaaat cccaaagctc taagcctgag 120

ctagggaggg tctcagaggg aggtctgact gcagaccggg agtcttctcc tcccgtgcgc 180

cgctgcccgg gacgagaaac ccgtggggca tccaggacta ggacacgagg tctcagcctg 240

ggcaggtgga caagctgtgg ggtcccaccc tccgcaggcg atggcttccc aaagtctgta 300

caaaccggtt tcgccgggcc ggccatgccc gcccctcttc tcggcgtggg aagccctttc 360

aaaagtggag gggagcgagt gtcgcgccct gccaaccccg actgcgcctg ggccctcccc 420

gcgccgggct ccggagccgc ccctcctgac tctgcgacca cggccgggga ccctgcgcgc 480

gcccgggaat gcagagtctc cagcgccgcg cagggctcgc cccgacctcg gccggccctg 540

ggcaacccgc tccgcggcca gtccccactc caagatgtgg ctcggctccc acctccgcgg 600

gggggaaatg tcgggcgacc cccacactga ccttcctgcg cacccagcgc aaactacgaa 660

cccagagttg gagctgcccg cagaccccgc gcagccagac cccgcgcctt tatcccgccc 720

cgccccgccc cgcccggcgc accaatcccc ggccgaggag gggccgcgtg gcgccgcggg 780

gggcgggccg cgcacgcccc ccgcagggag gactcaggga cagtcagggc cccgggagag 840

tccgcgcgca tcgcccggct ccgcggcgcc agccatggcg tccgtgcgtg gccccgccag 900

ggatggggcg acgcggtcag agccgcacgc gaccgaaatc cgcactctgg agccgcagag 960

cgcgcggtct tgctgtttag cggctccctg gcaagtgacg tggggaagaa acgcagggcg 1020

caggagagac agctggaaag gtttgcggtg tagctggccc aggattgagg gtctggaggt 1080

cgggtgttgg aagaccttga gcgaggcact tcttggcctc cccagctggg aggcatcgct 1140

gaaaaattag gtgaccccca agacggtaga ccagcagagt cagcgtcacc tgggcgccgg 1200

ttggaaatgc agattggcag gtcccacccc caacccctcc cgacttgctg agtcagcatc 1260

tctgggggtg gggctcgcgc gcccccagcg ggacgccggt 1300

<210> SEQ ID NO 157
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 157

ctcatttcgg gccgcttttc tcagagggca aagatgggtc agggtgggat gttacattag 60

tgttgagact ctttggatcc gtttcgtggg taccgaggac gcctgggtac gcgggacagg 120

ctgcacccgc ctgctagagg cgccccatcg aggcgccacg ggtgaagctc ccggccccac 180

ctacggggcg gggctccggc tcggtccgac tattgcccgc ggtgggggag ggggatggat 240

cacgccacgc gccaaaggcg atcgcgactc tccttctgca ggtagcctgg aaggctctct 300

ctctttctct acgccaccct tttcgtggca ctgaaaagcc ccgtcctctc ctcccagtcc 360

cgcctcctcc gagcgttccc cctactgcct ggaatggtgc ggtcccaggt cgcgggtcac 420

gcggcggagg gggcgtggcc tgcccccggc ccagccggct cttctttgcc tctgctggag 480

tccggggagt ggcgttggct gctagagcga tgccgggccg gagttgcgtc gccttagtcc 540

tcctggctgc cgccgtcagc tgtgccgtcg cgcagcacgc gccgccggtg agtgagcttg 600

agccgaggcg cagagagggg cgtgcaggtg cgggcgcgga tggaggcgca ggtgtggcgg 660 cgcgagcggg tacaaggaac acctcgtgct gggcagcttc tttacggggg tctgtggttt 720

cgtgcacagg ggtgtgggtg cagagcgggc tggcgaaccc cgtcctcggt agattcggtg 780

ctacctgcaa ctagaactcc 800

<210> SEQ ID NO 158
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 158

ggagttctag ttgcaggtag caccgaatct accgaggacg gggttcgcca gcccgctctg 60

cacccacacc cctgtgcacg aaaccacaga cccccgtaaa gaagctgccc agcacgaggt 120

gttccttgta cccgctcgcg ccgccacacc tgcgcctcca tccgcgcccg cacctgcacg 180

cccctctctg cgcctcggct caagctcact caccggcggc gcgtgctgcg cgacggcaca 240

gctgacggcg gcagccagga ggactaaggc gacgcaactc cggcccggca tcgctctagc 300

agccaacgcc actccccgga ctccagcaga ggcaaagaag agccggctgg gccgggggca 360

ggccacgccc cctccgccgc gtgacccgcg acctgggacc gcaccattcc aggcagtagg 420

gggaacgctc ggaggaggcg ggactgggag gagaggacgg ggcttttcag tgccacgaaa 480

agggtggcgt agagaaagag agagagcctt ccaggctacc tgcagaagga gagtcgcgat 540

cgcctttggc gcgtggcgtg atccatcccc ctccccccacc gcgggcaata gtcggaccga 600

gccggagccc cgccccgtag gtggggccgg gagcttcacc cgtggcgcct cgatggggcg 660

cctctagcag gcgggtgcag cctgtcccgc gtacccaggc gtcctcggta cccacgaaac 720

ggatccaaag agtctcaaca ctaatgtaac atcccaccct gacccatctt tgccctctga 780

gaaaagcggc ccgaaatgag 800

<210> SEQ ID NO 159
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 159

ttctgcagag ccagcagccg gctcccacct acccaaggag agaagatcgc tccaagacag 60

tgagagcttc cctgccattt cagtgcaaag tccctccgga gcgacctcag aggagtaacc 120

gggccttaac tttttgcgct cgttttgcta taatttttct ctatccacct ccatcccacc 180

cccacaacac tctttactgg gggggtcttt tgtgttccgg atctcccccct ccatggctcc 240

cttagccgaa gtcgggggct ttctgggcgg cctggagggc ttgggccagc aggtgggttc 300

gcatttcctg ttgcctcctg ccggggagcg gccgccgctg ctgggcgagc gcaggagcgc 360

ggcggagcgg agcgcgcgcg gcgggccggg ggctgcgcag ctggcgcacc tgcacggcat 420

cctgcgccgc cggcagctct attgccgcac cggcttccac ctgcagatcc tgcccgacgg 480

cagcgtgcag ggcacccggc aggaccacag cctcttcggt acgtactagc atcccgaccc 540

cacccccatc tgcgccccag ctcggctcct cgttccctcc ccttgcacct ccctctttgc 600

ctgccaaggg cgtcatcgcc gcgcggagcc cggagctccc ctggacccat ccggtgcaag 660

acgcaggctg gggctgaagg gctggccaga gcagccgcgg ggagaaattt tcctgctggt 720

ttgtcgccgc agcctctagc agggcagcag ctccagatgc tgggggcggg aggagaaagg 780

gtgggcgctt cgcaagctcc 800

<210> SEQ ID NO 160

<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 160

ggagcttgcg aagcgcccac cctttctcct cccgccccca gcatctggag ctgctgccct 60

gctagaggct gcggcgacaa accagcagga aaatttctcc ccgcggctgc tctggccagc 120

ccttcagccc cagcctgcgt cttgcaccgg atgggtccag gggagctccg ggctccgcgc 180

ggcgatgacg cccttggcag gcaaagaggg aggtgcaagg ggagggaacg aggagccgag 240

ctggggcgca gatgggggtg gggtcgggat gctagtacgt accgaagagg ctgtggtcct 300

gccgggtgcc ctgcacgctg ccgtcgggca ggatctgcag gtggaagccg gtgcggcaat 360

agagctgccg gcggcgcagg atgccgtgca ggtgcgccag ctgcgcagcc cccggcccgc 420

cgcgcgcgct ccgctccgcc gcgctcctgc gctcgcccag cagcggcggc cgctccccgg 480

caggaggcaa caggaaatgc gaacccacct gctggcccaa gccctccagg ccgcccagaa 540

agcccccgac ttcggctaag ggagccatgg agggggagat ccggaacaca aaagaccccc 600

ccagtaaaga gtgttgtggg ggtgggatgg aggtggatag agaaaaatta tagcaaaacg 660

agcgcaaaaa gttaaggccc ggttactcct ctgaggtcgc tccggaggga ctttgcactg 720

aaatggcagg gaagctctca ctgtcttgga gcgatcttct ctccttgggt aggtgggagc 780

cggctgctgg ctctgcagaa 800

<210> SEQ ID NO 161
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 161

cttaaccccc ccatctccag ttatcccaat gaaccgaccc cgagggggca tttccgctga 60

agtccggggc tgtaaaaaat taagtgagaa gagccgcgct aaagccaagc gtcgtcgtca 120

cccaaggtac tgcgctgatg cgctgcgggc cgaccaggtg ctcccgccgg ggcgtcttct 180

cctacgcagg aagggccacg ccgagagagg caggcaacaa gggcacggct ggaggccgga 240

aggtcacccc gtccccggcg gggcgggcgc ggcccagcct cacttcccgg gcacgttcgg 300

gcggggcgat tgcagggaac ggggcgggga ggcgacagtc cccggctccg ccgcgcgcca 360

gcccgccttc gctgcccgga ggcgccgcag gcctgggttc ccggacagct gagcccgagc 420

gccgcctccc gaaaggtgaa ggcggcccgg ggaggcgggg acggtgacgg gggcgggggc 480

cgcgggcggt ctcccgacgg ctgtcgcggg gccagcccaa agcccccgat ccccggtagc 540

tgcgcttccc gcgcggggcg ccggagtagg gcgggccaag ctggcctgcg gccgcggcgg 600

gaagaagggc tagcgaagca cccccgaccg ggcccaggcg ccggacgccg gggggcgcct 660

cgctgcaact tctctttgga agccccgaca cgagccccgg cccgcgcgcg cgctccccca 720

cggccacgcg cgcaccctgc cgcccgcacc cccgcgcgcc ctccgtctat tttttcctct 780

tcctttcatc ctcacactct aaaataggtc aaggggtgga agttacacct ggtgcagccc 840

tcggctctga tgcaaaagca gcttttgccc ctggctgcgg gacagcgctg tgactactcg 900

caacgggaga gctgctgcca gtcgccacac cgtgcggaaa gcgccggcga ccggagcact 960

gacaatggtc tgcatagggg agcggagaga agcttctgtt gcgccctaga tccgctgcct 1020

cggcgcccgc ccgcagggag gagggggcgc gacaggtcgt ctagcgcgtg ccccggagcc 1080

cgcgcccggg tctggccgcc tgggtgagtt cctgctcgtc ccctgccttt ccagtagccc 1140 ggggtggctg tttaccttgc aaacagcctt gcaatacgat caaaacaggc gagacagcca 1200

tgcagtaagg gattgcggga tgtgctttgg gtgtgagatt ggataaatca gaattcagag 1260

ataaaggaca tgtctagtgc cttaagggtt aaagtggatt 1300

<210> SEQ ID NO 162
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 162

aatccacttt aacccttaag gcactagaca tgtcctttat ctctgaattc tgatttatcc 60

aatctcacac ccaaagcaca tcccgcaatc ccttactgca tggctgtctc gcctgttttg 120

atcgtattgc aaggctgttt gcaaggtaaa cagccacccc gggctactgg aaaggcaggg 180

gacgagcagg aactcaccca ggcggccaga cccgggcgcg ggctccgggg cacgcgctag 240

acgacctgtc gcgcccctc ctccctgcgg gcgggcgccg aggcagcgga tctagggcgc 300

aacagaagct tctctccgct cccctatgca gaccattgtc agtgctccgg tcgccggcgc 360

tttccgcacg gtgtggcgac tggcagcagc tctcccgttg cgagtagtca cagcgctgtc 420

ccgcagccag ggcaaaagc tgcttttgca tcagagccga gggctgcacc aggtgtaact 480

tccacccctt gacctatttt agagtgtgag gatgaaagga agaggaaaaa atagacggag 540

ggcgcgcggg ggtgcgggcg gcagggtgcg cgcgtggccg tgggggagcg cgcgcgcggg 600

ccggggctcg tgtcggggct tccaaagaga agttgcagcg aggcgccccc cggcgtccgg 660

cgcctgggcc cggtcggggg tgcttcgcta gcccttcttc ccgccgcggc cgcaggccag 720

cttggcccgc cctactccgg cgccccgcgc gggaagcgca gctaccgggg atcgggggct 780

ttgggctggc cccgcgacag ccgtcgggag accgccccgcg gcccccgccc ccgtcaccgt 840

ccccgcctcc ccgggccgcc ttcacctttc gggaggcggc gctcgggctc agctgtccgg 900

gaacccaggc ctgcggcgcc tccgggcagc gaaggcgggc tggcgcgcgg cggagccggg 960

gactgtcgcc tccccgcccc gttccctgca atcgccccgc ccgaacgtgc ccgggaagtg 1020

aggctgggcc gcgcccgccc cgccggggac ggggtgacct tccggcctcc agccgtgccc 1080

ttgttgcctg cctctctcgg cgtggccctt cctgcgtagg agaagacgcc ccggcgggag 1140

cacctggtcg gcccgcagcg catcagcgca gtaccttggg tgacgacgac gcttggcttt 1200

agcgcggctc ttctcactta attttttaca gccccggact tcagcggaaa tgccccctcg 1260

gggtcggttc attgggataa ctggagatgg gggggttaag 1300

<210> SEQ ID NO 163
<211> LENGTH: 1800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 163

ctagcattta ctggattcca gagtcttgtt atttaagaat gcatcttaaa cggtactatc 60

aaattcatgt tacgtgcagc ccagattgtt ttgggcagca cgaaaagttt ctgaggcgct 120

gcgtgtaccc caccccagga caccgtgtgt gcgcgccgag ctgagtgcga ggaacgtggc 180

gcgagggccg ggggatgccg ggctgcgtgg gtgtgagccc tcgcgcgacc gcgaccccgc 240

gcctctcccg ctctcgccgg aacgtgaccg cagccgcacc tctcctccag ccctttccca 300

gccagacgct tccttttagg tccttctggg cgtttattgt aaattctgcg actaaaacac 360

gccggtgagc ccggcccacc gacagatgga tcaatcgccc ccttcccggc taggggagga 420

-continued

ggaacccccc aaccccggag cctagggagc cgggagctgc ctcgggacga gctcctcgga 480

gcccagccgg ctgcggagcc ccggcccggg tcggtctcgg ggccctcctg ccggggtggg 540

gtgcgagccc ctgcccgatt cctctggggc ggttcaggca ggtttgccgg cctccgagga 600

ggtggtcagg gcgccctggc ccagcaggct tcttcccgag ccgggggggag gggagaccgg 660

ctggggaagg ggcatctcga aggggtggag gccggggcgg gcgggaggca agcgcgccgc 720

gggcgtgagg gcaaagttcc cgaggtccgc gcggagagca cacgtgtatg tgcgcgcggg 780

gctaggccgg ggccggcagg atgcgttggg ttcgggggcg cgcggggccg gcgccgaagg 840

ggataattcc tttccctggc accatcgggg agacgctttg tcggcctcgg ctcctgggcg 900

cagggacgcc ttagcccacg gagggtggag cccccctcag acccgggcca ccggctgggg 960

tttttctaac gccctgcccc ccgagccccc ggatggctcg ggccccacgg actccgcgcc 1020

ctccagcctc agctcagctc cccaggcttc ccagacccag cggcgcaggg ggcgggggca 1080

ggggcagtgg gggttggagg gcgcagccgg tccccagggt ggggagagct gcgggggggag 1140

gaggaggagg gtgccgacgc ttgagtgggt tcgagcccga gccgtagccg gggagccag 1200

tcagtttccg gccaaggcag caggtcagtc ccaggaaggg cgggcgattg agccgaggga 1260

gccggcggct gggctctcct ctcggcccgc gatccccggc gccgccgccg ccgccaccgc 1320

caccgccacc gccttcgcct tgtcgccgcc gccgctgcag agcatcgtag ctccgccgcg 1380

ctcccgcgcc ccgcgccccg cgccgccagc cgcctgggag cccgagcgcc gagcccgggg 1440

cggaggagag gggcgctggc gcgagagccc gggcgaggga gccgcgaagg gagaaggggg 1500

cgggcggagg gaggagcagg gagagtggga gaagggggag ggagagagga gagcgaggga 1560

gagctggaga gagcgagagc aaagagcgag cgagggagag gagagagaga gagaggagag 1620

agaaagacac acgcacgcag agacacacgg tcactggaat tccattagaa aaaagtgagc 1680

cgagcaaggg ttagcgggag aagatttttt tgaatcttgt cttcgtcttg gtgcgaaaga 1740

agcgactcca gtctctcgtc ctcgaagctc cgactggatt gttcttgggc gctgacaccc 1800

<210> SEQ ID NO 164
<211> LENGTH: 1800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 164

gggtgtcagc gcccaagaac aatccagtcg gagcttcgag gacgagagac tggagtcgct 60

tctttcgcac caagacgaag acaagattca aaaaaatctt ctcccgctaa cccttgctcg 120

gctcactttt ttctaatgga attccagtga ccgtgtgtct ctgcgtgcgt gtgtctttct 180

ctctcctctc tctctctctc ctctccctcg ctcgctcttt gctctcgctc tctccagctc 240

tccctcgctc tcctctctcc ctcccccttc tcccactctc cctgctcctc cctccgcccg 300

ccccccttctc ccttcgcggc tccctcgccc gggctctcgc gccagcgccc ctctcctccg 360

ccccgggctc ggcgctcggg ctcccaggcg gctggcggcg cggggcgcgg ggcgcgggag 420

cgcggcggag ctacgatgct ctgcagcggc ggcggcgaca aggcgaaggc ggtggcggtg 480

gcggtggcgg cggcggcggc gccggggatc gcgggccgag aggagagccc agccgccggc 540

tccctcggct caatcgcccg cccttcctgg gactgacctg ctgccttggc cggaaactga 600

ctggctcccc cggctacggc tcgggctcga acccactcaa gcgtcggcac cctcctcctc 660

ctccccccgc agctctcccc accctgggga ccggctgcgc cctccaaccc ccactgcccc 720

tgccccccgcc ccctgcgccg ctgggtctgg gaagcctggg gagctgagct gaggctggag 780

-continued

```
ggcgcggagt ccgtggggcc cgagccatcc gggggctcgg ggggcagggc gttagaaaaa    840

ccccagccgg tggcccgggt ctgagggggg ctccaccctc cgtgggctaa ggcgtccctg    900

cgcccaggag ccgaggccga caaagcgtct ccccgatggt gccagggaaa ggaattatcc    960

ccttcggcgc cggccccgcg cgcccccgaa cccaacgcat cctgccggcc ccggcctagc   1020

cccgcgcgca catacacgtg tgctctccgc gcggacctcg ggaactttgc cctcacgccc   1080

gcggcgcgct tgcctcccgc ccgccccggc ctccacccct tcgagatgcc ccttccccag   1140

ccggtctccc ctccccccgg ctcgggaaga agcctgctgg gccagggcgc cctgaccacc   1200

tcctcggagg ccggcaaacc tgcctgaacc gccccagagg aatcgggcag gggctcgcac   1260

cccaccccgg caggagggcc ccgagaccga cccgggccgg ggctccgcag ccggctgggc   1320

tccgaggagc tcgtcccgag gcagctcccg gctccctagg ctccggggtt gggggggttcc   1380

tcctccccta gccgggaagg gggcgattga tccatctgtc ggtgggccgg gctcaccggc   1440

gtgttttagt cgcagaattt acaataaacg cccagaagga cctaaaagga agcgtctggc   1500

tgggaaaggg ctggaggaga ggtgcggctg cggtcacgtt ccggcgagag cgggagaggc   1560

gcggggtcgc ggtcgcgcga gggctcacac ccacgcagcc cggcatcccc cggccctcgc   1620

gccacgttcc tcgcactcag ctcggcgcgc acacacggtg tcctggggtg gggtacacgc   1680

agcgcctcag aaacttttcg tgctgcccaa aacaatctgg gctgcacgta acatgaattt   1740

gatagtaccg tttaagatgc attcttaaat aacaagactc tggaatccag taaatgctag   1800


<210> SEQ ID NO 165
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 165

aaacagcatt agccttctcc catcaaaagt ccggaagctg cccttcagtc gtcaaagtgt     60

ttgccttaat ttgcaatcgt tatgacttga gccaaatgct tatacctcat ttgtgtcgta    120

tatgtgaaga tacaattgca aatcgttcac gaccttgagt caagaccttg agtttcctga    180

ggtcaggaga ccgttaggga atgtgagtgt cccagacggg cgctgagccc agctcggaga    240

cccaccccgc ccgtagcagc ggcgcgggcc ccagagagcc ccgcactcgg ccgcgcctca    300

gttacgctga ctcggctgtg cccgcagtgt cgcgctgtcg cgtagccagg tgtcgccggg    360

ctggcgcggt tatttatgac tgcgtggttg ggctgggggt tcggggccgg ggagcagccg    420

ggatccgccg cctcttccat gatcttcccg ggccgaacca cgggaccgct acgctgaagg    480

tggcgtcgcg ggtccccggg gccgcgcgag tgtaggggtc gctctcggcc ggccgcgaag    540

ctcgcggcac cgacttctcg cgagatttcg gcgaccccccc cccccgcccc cgcccctccg    600

ttctctgccc cctcccagct ctggtgtggg cggcctccgc tatggctgcg ctgcgaaggc    660

tcttgtggcc gccaccccgg gtgtctcctc cactctgcgc tcaccagccc ctccttgggc    720

cgtgggggcg gcctgcggtg accaccctgg gccttcctgg ccggcccttc tcctcccgag    780

aggatgagga gagggctgtg gcggaggcgg catggaggcg gcggcggcgc tgggggggagc    840

tgagcgtggc ggcggcggcc ggcgggggggc tggtcggcct ggtatgctac cagctgtacg    900

gggaccccag ggccggctcg ccggcgaccg ggcgaccctc aaagagcgcg gccacggagc    960

ccgaggaccc gccccgcggc cgggggatgc tgcccatccc agtggcggct gccaaggaga   1020

cggtgagtgc gcgagcgcgc gtcacacctg cgcgggggat gtgaccttcg tgccgggtac   1080

gcaggaccct ggaggctgtg gggacggtgc aagcgctgtg gccgcgggtg aggaacttcc   1140
```

cgtgagcgag gctgacacct aggccggaca gcctaggatc cggtcaccca cgtattggga 1200

agaccagtga tgctgtccct gatgcatcag gaccttaaag gtggctgcag ctaccaagta 1260

tcaatccaaa cccaaaacca acacccctcc ccctcttaca 1300

<210> SEQ ID NO 166
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 166

tgtaagaggg ggaggggtgt tggttttggg tttggattga tacttggtag ctgcagccac 60

ctttaaggtc ctgatgcatc agggacagca tcactggtct tcccaatacg tgggtgaccg 120

gatcctaggc tgtccggcct aggtgtcagc ctcgctcacg ggaagttcct cacccgcggc 180

cacagcgctt gcaccgtccc cacagcctcc agggtcctgc gtacccggca cgaaggtcac 240

atcccccgcg caggtgtgac gcgcgctcgc gcactcaccg tctccttggc agccgccact 300

gggatgggca gcatcccccg gccgcggggc gggtcctcgg gctccgtggc cgcgctcttt 360

gagggtcgcc cggtcgccgg cgagccggcc ctggggtccc cgtacagctg gtagcatacc 420

aggccgacca gccccccgcc ggccgccgcc gccacgctca gctcccccca gcgccgccgc 480

cgcctccatg ccgcctccgc cacagccctc tcctcatcct ctcgggagga gaagggccgg 540

ccaggaaggc ccagggtggt caccgcaggc cgcccccacg gcccaaggag gggctggtga 600

gcgcagagtg gaggagacac ccggggtggc ggccacaaga gccttcgcag cgcagccata 660

gcggaggccg cccacaccag agctgggagg gggcagagaa cggaggggcg ggggcggggg 720

ggggggtcgc cgaaatctcg cgagaagtcg gtgccgcgag cttcgcggcc ggccgagagc 780

gacccctaca ctcgcgcggc cccggggacc cgcgacgcca ccttcagcgt agcggtcccg 840

tggttcggcc cgggaagatc atggaagagg cggcggatcc cggctgctcc ccggccccga 900

acccccagcc caaccacgca gtcataaata accgcgccag cccggcgaca cctggctacg 960

cgacagcgcg acactgcggg cacagccgag tcagcgtaac tgaggcgcgg ccgagtgcgg 1020

ggctctctgg ggcccgcgcc gctgctacgg gcggggtggg tctccgagct gggctcagcg 1080

cccgtctggg acactcacat tccctaacgg tctcctgacc tcaggaaact caaggtcttg 1140

actcaaggtc gtgaacgatt tgcaattgta tcttcacata tacgacacaa atgaggtata 1200

agcatttggc tcaagtcata acgattgcaa attaaggcaa acactttgac gactgaaggg 1260

cagcttccgg acttttgatg ggagaaggct aatgctgttt 1300

<210> SEQ ID NO 167
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 167

cctggcgcgg acaggaccca gaaacaaacc acagcccggg gcgcagccgc cagggcgaag 60

gttagttccg gtcccttccc ctcccctccc cacttggacg cgcttgcgga ggattgcgtt 120

gacgagactc ttatttattg tcaccaacct gtggtggaat ttgcagttgc acattggatc 180

tgattcgccc cgccccgaat gacgcctgcc cggaggcagt gaaagtacag ccgcgccgcc 240

ccaagtcagc ctggacacat aaatcagcac gcggccggag aaccccgcaa tctctgcgcc 300

cacaaaatac accgacgatg cccgatctac tttaagggct gaaacccacg ggcctgagag 360

actataagag cgttccctac cgccatggaa caacggggac agaacgcccc ggccgcttcg 420

-continued

ggggcccgga aaaggcacgg cccaggaccc agggaggcgc ggggagccag gcctgggccc 480

cgggtcccca agacccttgt gctcgttgtc gccgcggtcc tgctgttggt gagtccccgc 540

cgcggtccct ggctggggaa gagcgtgcct ggcgcctgga gagggcaggg agagaggggg 600

acacggcggg ggtgcgtggc ccgggtcgcc tgcggccggg catgtccggg caagacgcac 660

cagtcgtcgg agtcggggga agagatgggt ccccgggttg ggcaggagcg acctgggccg 720

ccagggaaca gagcgcgcgc tccacttggt gtaaattccc gaatccagtg ggggagggcg 780

acaaggaggg aattcccgag taagctgcgt gaagccacgg agaggtcgtc ggactttgat 840

tttgttttct ttccttactt tctgtttctt tctctttttc tctttcttcc tttctttccc 900

tcccttcctt cctcgctcag ttcctgcctt aatttctttt tcttttgcgc cttcgaatga 960

attcctaaag gcgctcattg cagatcgctt tgaacctgcg gccggcgaag aactcccctg 1020

tggtcgctgc ggcccagtgg ttccgttccg tgcgcgggag tcgtcgcggg cgcagctgga 1080

gaggcccctt cccctcctta gcggctgcgc ccctacgcgt gcggggccgc tcatcgccaa 1140

tgccattgtt tggggttcct tgggaaaacg agatttagga gaagggagtt gtggcacttg 1200

gggcctgacc tgcttgataa tagcagctgc attttggcct gggaagagcc tttcttgcca 1260

cctcttggca agtatccgtg ataatgggga agggacaaag 1300

<210> SEQ ID NO 168
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 168

ctttgtccct tccccattat cacggatact tgccaagagg tggcaagaaa ggctcttccc 60

aggccaaaat gcagctgcta ttatcaagca ggtcaggccc caagtgccac aactcccttc 120

tcctaaatct cgttttccca aggaacccca aacaatggca ttggcgatga gcggccccgc 180

acgcgtaggg gcgcagccgc taaggagggg aaggggcctc tccagctgcg cccgcgacga 240

ctcccgcgca cggaacggaa ccactgggcc gcagcgacca caggggagtt cttcgccggc 300

cgcaggttca aagcgatctg caatgagcgc ctttaggaat tcattcgaag gcgcaaaaga 360

aaaagaaatt aaggcaggaa ctgagcgagg aaggaaggga gggaaagaaa ggaagaaaga 420

gaaaaagaga aagaaacaga aagtaaggaa agaaaacaaa atcaaagtcc gacgacctct 480

ccgtggcttc acgcagctta ctcgggaatt ccctccttgt cgccctcccc cactggattc 540

gggaatttac accaagtgga gcgcgcgctc tgttccctgg cggcccaggt cgctcctgcc 600

caacccgggg acccatctct tcccccgact ccgacgactg gtgcgtcttg cccggacatg 660

cccggccgca ggcgacccgg gccacgcacc cccgccgtgt ccccctctct ccctgccctc 720

tccaggcgcc aggcacgctc ttccccagcc agggaccgcg gcggggactc accaacagca 780

ggaccgcggc gacaacgagc acaagggtct tggggacccg ggcccaggc ctggctcccc 840

gcgcctccct gggtcctggg ccgtgccttt tccgggcccc cgaagcggcc ggggcgttct 900

gtccccgttg ttccatggcg gtagggaacg ctcttatagt ctctcaggcc cgtgggtttc 960

agcccttaaa gtagatcggg catcgtcggt gtattttgtg ggcgcagaga ttgcggggtt 1020

ctccggccgc gtgctgattt atgtgtccag gctgacttgg ggcggcgcgg ctgtactttc 1080

actgcctccg ggcaggcgtc attcggggcg gggcgaatca gatccaatgt gcaactgcaa 1140

attccaccac aggttggtga caataaataa gagtctcgtc aacgcaatcc tccgcaagcg 1200

cgtccaagtg gggaggggag gggaagggac cggaactaac cttcgccctg gcggctgcgc 1260 cccgggctgt ggtttgtttc tgggtcctgt ccgcgccagg 1300

<210> SEQ ID NO 169
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 169

tgcccctttt ctgagtgctt ggaagtgact gctgcaagtg acaagtgacc acgccttttc 60

ccccgcgggt ataaattcag aggcgctgcg ctccgattct ggcagtgcag ctgtgggaac 120

ctctccacgc gcacgaactc agccaacgat ttctgataga tttttgggag tttgaccaga 180

gatgcaaggg gtgaaggagc gcttcctacc gttagggaac tctggggaca gagcgccccg 240

gccgcctgat ggccgaggca gggtgcgacc caggacccag gacggcgtcg ggaaccatac 300

catggcccgg atccccaaga ccctaaagtt cgtcgtcgtc atcgtcgcgg tcctgctgcc 360

agtgagtccc ggccgcggtc cctggctggg gaagagcgca cctggcgccg ggagggggca 420

gggagacggg gacacggcag ggatgcctgg ccctggtcac ctgcggccgg gcatgtccgg 480

gcaggacgaa ctcgccgtcg gagtcagggg aagaactggg tccccgggct gggcaggagg 540

gacccggccg cgagggagca gagaggcggt ccccctggct gccccgagcc cgcgaaggga 600

gggaagttcc agaatcgaga gagggaggga gtcaaggtgg aacccataga gtgagcctcc 660

tgaagacaca gagcggttgc ctctctcatt aattaattaa ttagttaata aaattaaccc 720

catgtttaca ttcttaaacg tgttccttgg agatcggttt aaccaacagc cagtgaaaaa 780

acttttcagc gctgtcttta 800

<210> SEQ ID NO 170
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 170

taaagacagc gctgaaaagt tttttcactg gctgttggtt aaaccgatct ccaaggaaca 60

cgtttaagaa tgtaaacatg ggttaattt tattaactaa ttaattaatt aatgagagag 120

gcaaccgctc tgtgtcttca ggaggctcac tctatgggtt ccaccttgac tccctccctc 180

tctcgattct ggaacttccc tcccttcgcg ggctcggggc agccaggggg accgcctctc 240

tgctccctcg cggccgggtc cctcctgccc agcccgggga cccagttctt cccctgactc 300

cgacggcgag ttcgtcctgc ccggacatgc ccggccgcag gtgaccaggg ccaggcatcc 360

ctgccgtgtc cccgtctccc tgccccctcc cggcgccagg tgcgctcttc cccagccagg 420

gaccgcggcc gggactcact ggcagcagga ccgcgacgat gacgacgacg aactttaggg 480

tcttggggat ccgggccatg gtatggttcc cgacgccgtc ctgggtcctg ggtcgcaccc 540

tgcctcggcc atcaggcggc cggggcgctc tgtccccaga gttccctaac ggtaggaagc 600

gctccttcac cccttgcatc tctggtcaaa ctcccaaaaa tctatcagaa atcgttggct 660

gagttcgtgc gcgtggagag gttcccacag ctgcactgcc agaatcggag cgcagcgcct 720

ctgaatttat acccgcgggg gaaaaggcgt ggtcacttgt cacttgcagc agtcacttcc 780

aagcactcag aaaaggggca 800

<210> SEQ ID NO 171
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 171

gaaataactt gagccaggga tcaaacacta agattggcag gaaatgagca ggaagaggta 60

gcggggtccc tgacgccatc tattcaattg tttttcagaa gaggtatcag ctcttgaagg 120

cttacttctc aatactggct gcgagagcaa gaatggtgtg taatttacaa aagccgtcat 180

tgctgtaggt aagttgtagc aaacgactcg cgcccgagca ttcccgcccc cgccttcgct 240

gcggccccgc ccacgacgac cctggggaac tacaagtccc gccatacagc ggggagcgcc 300

cggagctcgc gccggccccg cccccagccc ggtccccacc cccggctccg cccccggccc 360

cctcccgccg ggtcaacccc gaagagtcgc cggtggccgc ggcagacgga agccgaacga 420

gttcctcggc ggctgcagga tgggggactc caaagtgaaa gtggcggtgc ggatacgacc 480

catgaaccgg cgaggtgaga gccgagccct cctgggccgc cggggcggag gcggcaggtg 540

cctggcgcgc ccttccctcg gccgccgtgg ggggtccggc ggccccgccc ctatagtcag 600

cggcggggcg cgaggagggg cccggggacc ctgaaacccg ctcccgcgct gagacgcccg 660

gctccctctt ctcccctccc ttccccccctg gccagccccg tccctggcgc cgtcgggccc 720

ctcgtgccgg ccccgctgcc ccttccgcct gcgcccgccc cgcccctgcg ccctttttgcc 780

ctctcgtctc ccccggaggt tcccgagggc gccctcggcc ctcgcgccca gcctcgtcct 840

ggcccctcag cctcgctcct tccccgccag ctgtcatcgt cgcccccgcg cgcgggtcgc 900

cagcccctgc agcccgcctc gggaccgccc gggacccccc gggaccccgc gtctcgcccg 960

ggtcgcccaa gcctgcaccg ccttggcccg cggcgggaag aagggcaggg ggccaggcgg 1020

gtgccccgcg gcgagttcct tccacctggg cgtcctgaga ttggggtcag gtggaggaga 1080

tgccctttttc gttgtttttg gacagttgag aaagttttgg ttttgcctga agtctcattc 1140

atcatctctc aataaatagc taaagtgcca agattcttgt ggaattgtat ctttctgaca 1200

ttctcttaac tctgcaggga gtgtagagaa ggcagataaa ccgagtacat ttaaataatc 1260

tgtagacccg gggagtggag agaaccccaa aagtcagggg 1300

<210> SEQ ID NO 172
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 172

cccctgactt ttggggttct ctccactccc cgggtctaca gattatttaa atgtactcgg 60

tttatctgcc ttctctacac tccctgcaga gttaagagaa tgtcagaaag atacaattcc 120

acaagaatct tggcacttta gctatttatt gagagatgat gaatgagact tcaggcaaaa 180

ccaaaacttt ctcaactgtc caaaaacaac gaaaagggca tctcctccac ctgaccccaa 240

tctcaggacg cccaggtgga aggaactcgc cgcggggcac ccgcctggcc ccctgccctt 300

cttcccgccg cgggccaagg cggtgcaggc ttgggcgacc cgggcgagac gcggggtccc 360

ggggggtccc gggcggtccc gaggcgggct gcaggggctg gcgacccgcg cgcgggggcg 420

acgatgacag ctggcgggga aggagcgagg ctgaggggcc aggacgaggc tgggcgcgag 480

ggccgagggc gccctcggga acctccgggg gagacgagag ggcaaaaggg cgcaggggcg 540

gggcgggcgc aggcggaagg ggcagcgggg ccggcacgag gggcccgacg gcgccaggga 600

cggggctggc cagggggggaa gggaggggag aagagggagc cgggcgtctc agcgcgggag 660

cgggtttcag ggtccccggg cccctcctcg cgccccgccg ctgactatag ggcggggcc 720

gccggacccc ccacggcggc cgagggaagg gcgcgccagg cacctgccgc ctccgccccg 780 gcggcccagg agggctcggc tctcacctcg ccggttcatg ggtcgtatcc gcaccgccac   840

tttcactttg gagtccccca tcctgcagcc gccgaggaac tcgttcggct tccgtctgcc   900

gcggccaccg gcgactcttc ggggttgacc cggcgggagg gggccggggg cggagccggg   960

ggtggggacc gggctggggg cggggccggc gcgagctccg ggcgctcccc gctgtatggc   1020

gggacttgta gttccccagg gtcgtcgtgg gcggggccgc agcgaaggcg gggcgggaa   1080

tgctcgggcg cgagtcgttt gctacaactt acctacagca atgacggctt ttgtaaatta   1140

cacaccattc ttgctctcgc agccagtatt gagaagtaag ccttcaagag ctgatacctc   1200

ttctgaaaaa caattgaata gatggcgtca gggaccccgc tacctcttcc tgctcatttc   1260

ctgccaatct tagtgtttga tccctggctc aagttatttc   1300

<210> SEQ ID NO 173
<211> LENGTH: 1550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 173

acccccctcct tccttctttc cctaccgccc cacgcgcgac ccggggatgg ctccgtggcc   60

tcacgagaac agctctcttg ccccatggcc ggacctcccc accctggcgc ccaataccgc   120

caacaccagt gggctgccag gggttccgtg ggaggcggcc ctagccgggg ccctgctggc   180

gctggcggtg ctggccaccg tgggaggcaa cctgctggtc atcgtggcca tcgcctggac   240

tccgagactc cagaccatga ccaacgtgtt cgtgacttcg ctggccgcag ccgacctggt   300

gatgggactc ctggtggtgc cgccggcggc caccttggcg ctgactggcc actggccgtt   360

gggcgccact ggctgcgagc tgtggacctc ggtggacgtg ctgtgtgtga ccgccagcat   420

cgaaaccctg tgcgccctgg ccgtggaccg ctacctggct gtgaccaacc cgctgcgtta   480

cggcgcactg gtcaccaagc gctgcgcccg gacagctgtg gtcctggtgt gggtcgtgtc   540

ggccgcggtg tcgtttgcgc ccatcatgag ccagtggtgg cgcgtagggg ccgacgccga   600

ggcgcagcgc tgccactcca acccgcgctg ctgtgccttc gcctccaaca tgccctacgt   660

gctgctgtcc tcctccgtct ccttctacct tcctcttctc gtgatgctct tcgtctacgc   720

gcgggttttc gtggtggcta cgcgccagct gcgcttgctg cgcggggagc tgggccgctt   780

tccgcccgag gagtctccgc cggcgccgtc gcgctctctg gccccggccc cggtggggac   840

gtgcgctccg cccgaagggg tgcccgcctg cggccggcgg cccgcgcgcc tcctgcctct   900

ccgggaacac cgggccctgt gcaccttggg tctcatcatg ggcaccttca ctctctgctg   960

gttgcccttc tttctggcca acgtgctgcg cgccctgggg ggcccctctc tagtcccggg   1020

cccggctttc cttgccctga actggctagg ttatgccaat tctgccttca acccgctcat   1080

ctactgccgc agcccggact ttcgcagcgc cttccgccgt cttctgtgcc gctgcggccg   1140

tcgcctgcct ccggagccct gcgccgccgc ccgcccggcc ctcttcccct cgggcgttcc   1200

tgcggcccgg agcagcccag cgcagcccag gctttgccaa cggctcgacg ggtaggtaac   1260

cggggcagag ggaccggcgg ctcagggtcg ggaagcatgc gatgtgtccg tgggtcaact   1320

ttttgagtgt ggagtttatt aagagaaggt gggatggctt tgcttggaga gaaaagggaa   1380

cgaggagtag cgaaccaaaa tgggacccag ggtccttttc tttccggatc cagtcactag   1440

ggtagaagca aaggagggcg agcgggccgt cgttcctcac ccaaggaccc aaggtgcgcc   1500

accggaaagc gctgcggtgt cccgaggact ctcgcctcgc ctggtcggct   1550

<210> SEQ ID NO 174

<211> LENGTH: 1550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 174

agccgaccag gcgaggcgag agtcctcggg acaccgcagc gctttccggt ggcgcacctt 60

gggtccttgg gtgaggaacg acggcccgct cgccctcctt tgcttctacc ctagtgactg 120

gatccggaaa gaaaaggacc ctgggtccca ttttggttcg ctactcctcg ttccctttttc 180

tctccaagca aagccatccc accttctctt aataaactcc acactcaaaa agttgaccca 240

cggacacatc gcatgcttcc cgaccctgag ccgccggtcc ctctgccccg gttacctacc 300

cgtcgagccg ttggcaaagc ctgggctgcg ctgggctgct ccgggccgca ggaacgcccg 360

aggggaagag ggccgggcgg gcggcggcgc agggctccgg aggcaggcga cggccgcagc 420

ggcacagaag acggcggaag gcgctgcgaa agtccgggct gcggcagtag atgagcgggt 480

tgaaggcaga attggcataa cctagccagt tcagggcaag gaaagccggg cccgggacta 540

gagaggggcc ccccagggcg cgcagcacgt tggccagaaa gaagggcaac cagcagagag 600

tgaaggtgcc catgatgaga cccaaggtgc acagggcccg gtgttcccgg agaggcagga 660

ggcgcgcggg ccgccggccg caggcgggca ccccttcggg cggagcgcac gtccccaccg 720

gggccggggc cagagagcgc gacggcgccg gcggagactc ctcgggcgga aagcggccca 780

gctccccgcg cagcaagcgc agctggcgcg tagccaccac gaaaacccgc gcgtagacga 840

agagcatcac gagaagagga aggtagaagg agacggagga ggacagcagc acgtagggca 900

tgttggaggc gaaggcacag cagcgcgggt tggagtggca gcgctgcgcc tcggcgtcgg 960

cccctacgcg ccaccactgg ctcatgatgg gcgcaaacga caccgcggcc gacacgaccc 1020

acaccaggac cacagctgtc cgggcgcagc gcttggtgac cagtgcgccg taacgcagcg 1080

ggttggtcac agccaggtag cggtccacgg ccagggcgca cagggtttcg atgctggcgg 1140

tcacacacag cacgtccacc gaggtccaca gctcgcagcc agtggcgccc aacggccagt 1200

ggccagtcag cgccaaggtg gccgccggcg gcaccaccag gagtcccatc accaggtcgg 1260

ctgcggccag cgaagtcacg aacacgttgg tcatggtctg gagtctcgga gtccaggcga 1320

tggccacgat gaccagcagg ttgcctccca cggtggccag caccgccagc gccagcaggg 1380

ccccggctag ggccgcctcc cacggaaccc ctggcagccc actggtgttg gcggtattgg 1440

gcgccagggt ggggaggtcc ggccatgggg caagagagct gttctcgtga ggccacggag 1500

ccatccccgg gtcgcgcgtg ggcggtaggg gaaagaagga aggagggggt 1550

<210> SEQ ID NO 175
<211> LENGTH: 1800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 175

cgcagaccca gcaggagagc gcaacctagc atctttaagg ttcgcttagc ccttcctgtg 60

cacctggaag gaagccttat cttaaactcc cttccaccta gagtttattt tcgcctgcgt 120

gcgacagggc ttttgtactt aagtgagtta aggaatgaac cccgaactct tctgggaaag 180

ccaccaacgt tccccccgca cccctcccag ggttcctgac cacggagact ctgcttgggg 240

cacaggtgtg ggagtcgcaa acttttctct gcgccgtcct tttccgcgtg gaatgggacg 300

gagcagccct cccaggcgct gcctggctgc ggaggggagc gggcagcgag agcctcgggt 360

ctccgcctgg gttcccgggt ctccggggcg ctggcctcgg tctccgcgca gcgtccagcg 420 acccctgtcg ggggttcccg gcagccgcgc cgccaccccc cgcccggcca gcgcgggagg 480

aaaaggggct gcgcccggga gcgccgagcc caggctcctc ccggtggcgt gtccgcgcct 540

cggggtgggg gtgtggtggg gaagagggag ggggcgaggc caggggaggg tgcgaaggag 600

gcgcctgcct ccaacctgcg ggcgggaggt gggtggctgc ggggcaattg aaaaagagcc 660

ggcgaggagt tccccgaaac ttgttggaac tccgggctcg cgcggaggcc aggagctgag 720

cggcggcggc tgccggacga tgggagcgtg agcaggacgg tgataacctc tccccgatcg 780

ggttgcgagg gcgccgggca gaggccagga cgcgagccgc cagcggtggg acccatcgac 840

gacttcccgg ggcgacagga gcagccccga gagccagggc gagcgcccgt tccaggtggc 900

cggaccgccc gccgcgtccg cgccgcgctc cctgcaggca acgggagacg cccccgcgca 960

gcgcgagcgc ctcagcgcgg ccgctcgctc tccccctcga gggacaaact tttcccaaac 1020

ccgatccgag cccttggacc aaactcgcct gcgccgagag ccgtccgcgt agagcgctcc 1080

gtctccggcg agatgtccga gcgcaaagaa ggcagaggca aagggaaggg caagaagaag 1140

gagcgaggct ccggcaagaa gccggagtcc gcggcgggca gccagagccc aggtgggtgc 1200

gcagcgcggc ccgggcccca cgatcctcct cctgctcctc ctactcctcc tcctcctcgg 1260

atgccgtggc ctctccctcc ccctctccct cgcccgtcct cttcgccctg cgctctgagc 1320

gcccgttgag tcgcgcggtg cttcccctcc tgggggccgc cgctcacctg ggcgccgagt 1380

cctaccgggc gcctacgccc agagctcagg gcaagggaca gcagtcccgg ccgcaccctc 1440

ccagagtccc gggagcgctt cgctccctgg cacggcccct ccccagcgcc ttagcggctg 1500

agcccagccc gggagtggga cctgggctat aggagtcgag gctgcgtgcg cgcgtgcccc 1560

gcgccataag cgctttgcac gggggccgtg tgccctctag cgggaaacgc tggaatgggc 1620

cgcctggagg gagagccggt cccctcggtg tgcctggcag cgcagaagtg ggtggtcgag 1680

caagaggccg cgtgggaagt tagcttcggc gttttggggc acagggcaag cgatgtagag 1740

tgcgcgccgg ttcatcttga ttcagtcctg tgctacggag actcaagagc agcggcaggg 1800

<210> SEQ ID NO 176
<211> LENGTH: 1800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 176

ccctgccgct gctcttgagt ctccgtagca caggactgaa tcaagatgaa ccggcgcgca 60

ctctacatcg cttgccctgt gccccaaaac gccgaagcta acttcccacg cggcctcttg 120

ctcgaccacc cacttctgcg ctgccaggca caccgagggg accggctctc cctccaggcg 180

gcccattcca gcgtttcccg ctagagggca cacggccccc gtgcaaagcg cttatggcgc 240

ggggcacgcg cgcacgcagc ctcgactcct atagcccagg tcccactccc gggctgggct 300

cagccgctaa ggcgctgggg aggggccgtg ccagggagcg aagcgctccc gggactctgg 360

gagggtgcgg ccgggactgc tgtcccttgc cctgagctct gggcgtaggc gcccggtagg 420

actcggcgcc caggtgagcg gcggccccca ggaggggaag caccgcgcga ctcaacgggc 480

gctcagagcg cagggcgaag aggacgggcg agggagaggg ggagggagag gccacggcat 540

ccgaggagga ggaggagtag gaggagcagg aggaggatcg tggggcccgg gccgcgctgc 600

gcacccacct gggctctggc tgcccgccgc ggactccggc ttcttgccgg agcctcgctc 660

cttcttcttg cccttccctt tgcctctgcc ttctttgcgc tcggacatct cgccggagac 720

ggagcgctct acgcggacgg ctctcggcgc aggcgagttt ggtccaaggg ctcggatcgg 780

-continued

gtttgggaaa agtttgtccc tcgaggggga gagcgagcgg ccgcgctgag gcgctcgcgc 840

tgcgcggggg cgtctcccgt tgcctgcagg gagcgcggcg cggacgcggc gggcggtccg 900

gccacctgga acgggcgctc gccctggctc tcggggctgc tcctgtcgcc ccgggaagtc 960

gtcgatgggt cccaccgctg gcggctcgcg tcctggcctc tgcccggcgc cctcgcaacc 1020

cgatcgggga gaggttatca ccgtcctgct cacgctccca tcgtccggca gccgccgccg 1080

ctcagctcct ggcctccgcg cgagcccgga gttccaacaa gtttcgggga actcctcgcc 1140

ggctcttttt caattgcccc gcagccaccc acctcccgcc cgcaggttgg aggcaggcgc 1200

ctccttcgca ccctcccctg gcctcgcccc ctccctcttc cccaccacac ccccaccccg 1260

aggcgcggac acgccaccgg gaggagcctg ggctcggcgc tcccgggcgc agccccttttt 1320

cctcccgcgc tggccgggcg gggggtggcg gcgcggctgc cgggaacccc cgacaggggt 1380

cgctggacgc tgcgcggaga ccgaggccag cgccccggag acccgggaac ccaggcggag 1440

acccgaggct ctcgctgccc gctcccctcc gcagccaggc agcgcctggg agggctgctc 1500

cgtcccattc cacgcggaaa aggacggcgc agagaaaagt ttgcgactcc cacacctgtg 1560

ccccaagcag agtctccgtg gtcaggaacc ctgggagggg tgcgggggga acgttggtgg 1620

ctttcccaga agagttcggg gttcattcct taactcactt aagtacaaaa gccctgtcgc 1680

acgcaggcga aaataaactc taggtggaag ggagtttaag ataaggcttc cttccaggtg 1740

cacaggaagg gctaagcgaa ccttaaagat gctaggttgc gctctcctgc tgggtctgcg 1800

<210> SEQ ID NO 177
<211> LENGTH: 1550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 177

gggagggtgg cctgcaaggc ggggccggtt gcggtcaagt tcaagtaggg tcagagcagg 60

agaacactgg cataaaaaat agccacatcc aaggaagcag tgaggtgtgg ggaccatcta 120

tttcggtggg ccttcccacc cccaggccgg ccttcccatc acgcgtgggt gtgggggcac 180

tgcccccgct gcgcgcagga acagcgggga gagccaggag cggagcggct tcgggatgcc 240

agactgagca gtgggttcgt ctgcggccac ctctcaggga acaagcttcc ccccgcggag 300

actctgcttc ttttaaaagc cttcctgggt ttagtctagg gcgacaggac gacctccctt 360

gggaagggag agcctgccag tccccctccc attcgccagg cggtgcagcc cctcctcccg 420

cccggggcgc gcgcacctca gcgtcgcggg cctagcgccc agcagccgcg ccccaggccg 480

ggcctcgggt tccgggagcc cgcaggcgcg cgcccggccg ggcgtgtcgg gagcgcgcgg 540

cggccggggg cggagcgcag ccagggctgc gcggcgcgcc ccggctcccg cccgctccca 600

gccgggcccc ccagcggtcg gcgggacggc tcccggctgc agtctgcccg cccgccccgc 660

gcgggggccg agtcgcgaag cgcgcctgcg acccggcgtc cgggcgcgct ggagaggacg 720

cgaggagcca tgaggcgcca gcctgcgaag gtggcggcgc tgctgctcgg gctgctcttg 780

gaggtagggg ccggggaccg ggtgctgccg gaggcgcggc gcccaccatg ctggcggctg 840

ggggcgcgca gttccgaggc gccccagagg accttgcctg ggagcgcaga cggtggagcg 900

acggggagcc acagccctgc gcgcctcccg gagctgggag gtgcgggacc ctggtgacgg 960

ggaggctccc gccccggtcc gcgccttccg tcgttccttc ggttttcgca ccccgccccc 1020

accctgcggg tgagcgcgtt tcccgcgccg accgcctccg ttagctcggg gtgacctttg 1080

tgcaccgtcc gccccctctc cccgccgcag agggccgagg atcggatgga cccggggttg 1140 ggcgggggtg gtcctcgggc gcggcgcagg cgcggagagc ccggggcgcc gggcagtttg 1200

gggttaggaa aggatgggtg ccgagccggg gtgaggggag cgggcggagg ggactgtggg 1260

gaagtgtcgc gggagtgccg ggagttgtgg aggtgagcag cgggaggagg cgttcccgcg 1320

tgtgaaaatg aagtgcagcc tttaggtgcg gggaggaaat tctgcggaga gcctggctgg 1380

gtgggggtgc ggagccgaag ccggcgggga acttgttgag cggcttccgg gtgcgagcgc 1440

ccgtgaccgc atccctggcg gggaccgcgg ctgctcctgg ctgtgaaatt gcatcctcgg 1500

atggggccac atacttctca ctaaagcagg ttccttaaaa tgcgaactag 1550

<210> SEQ ID NO 178
<211> LENGTH: 1550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 178

ctagttcgca ttttaaggaa cctgctttag tgagaagtat gtggccccat ccgaggatgc 60

aatttcacag ccaggagcag ccgcggtccc cgccagggat gcggtcacgg gcgctcgcac 120

ccggaagccg ctcaacaagt tccccgccgg cttcggctcc gcacccccac ccagccaggc 180

tctccgcaga atttcctccc cgcacctaaa ggctgcactt cattttcaca cgcgggaacg 240

cctcctcccg ctgctcacct ccacaactcc cggcactccc gcgacacttc cccacagtcc 300

cctccgcccg ctcccctcac ccccgctcgg cacccatcct ttcctaaccc caaactgccc 360

ggcgccccgg gctctccgcg cctgcgccgc gcccgaggac cacccccgcc caaccccggg 420

tccatccgat cctcggccct ctgcggcggg gagaggggc ggacggtgca caaaggtcac 480

cccgagctaa cggaggcggt cggcgcggga aacgcgctca cccgcagggt gggggcgggg 540

tgcgaaaacc gaaggaacga cggaaggcgc ggaccggggc gggagcctcc ccgtcaccag 600

ggtcccgcac ctcccagctc cgggaggcgc gcagggctgt ggctccccgt cgctccaccg 660

tctgcgctcc caggcaaggt cctctggggc gcctcggaac tgcgcgcccc cagccgccag 720

catggtgggc gccgcgcctc cggcagcacc cggtccccgg cccctacctc caagagcagc 780

ccgagcagca gcgccgccac cttcgcaggc tggcgcctca tggctcctcg cgtcctctcc 840

agcgcgcccg gacgccgggt cgcaggcgcg cttcgcgact cggcccccgc gcggggcggg 900

cgggcagact gcagccggga gccgtcccgc cgaccgctgg ggggcccggc tgggagcggg 960

cgggagccgg ggcgcgccgc gcagccctgg ctgcgctccg cccccggccg ccgcgcgctc 1020

ccgacacgcc cggccgggcg cgcgcctgcg ggctcccgga acccgaggcc cggcctgggg 1080

cgcggctgct gggcgctagg cccgcgacgc tgaggtgcgc gcgccccggg cgggaggagg 1140

ggctgcaccg cctggcgaat gggaggggga ctggcaggct ctcccttccc aagggaggtc 1200

gtcctgtcgc cctagactaa acccaggaag gcttttaaaa gaagcagagt ctccgcgggg 1260

ggaagcttgt tccctgagag gtggccgcag acgaacccac tgctcagtct ggcatcccga 1320

agccgctccg ctcctggctc tccccgctgt tcctgcgcgc agcgggggca gtgcccccac 1380

acccacgcgt gatgggaagg ccggcctggg ggtgggaagg cccaccgaaa tagatggtcc 1440

ccacacctca ctgcttcctt ggatgtggct attttttatg ccagtgttct cctgctctga 1500

ccctacttga acttgaccgc aaccggcccc gccttgcagg ccaccctccc 1550

<210> SEQ ID NO 179
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 179

tgctgggcaa tgcgtgcgtg gtggctgcca tcgccttgga gcgctccctg cagaacgtgg 60

ccaattatct tattggctct ttggcggtca ccgacctcat ggtgtcggtg ttggtgctgc 120

ccatggccgc gctgtatcag gtgctcaaca agtggacact gggccaggta acctgcgacc 180

tgttcatcgc cctcgacgtg ctgtgctgca cctcatccat cttgcacctg tgcgccatcg 240

cgctggacag gtactgggcc atcacggacc ccatcgacta cgtgaacaag aggacgcccc 300

ggcgcgccgc tgcgctcatc tcgctcactt ggcttattgg cttcctcatc tctatcccgc 360

ccatgctggg ctggcgcacc ccggaagacc gctcggaccc cgacgcatgc accattagca 420

aggatcatgg ctacactatc tattccacct ttggagcttt ctacatcccg ctgctgctca 480

tgctggttct ctatgggcgc atattccgag ctgcgcgctt ccgcatccgc aagacggtca 540

aaaaggtgga gaagaccgga gcggacaccc gccatggagc atctcccgcc ccgcagccca 600

agaagagtgt gaatggagag tcggggagca ggaactggag gctgggcgtg gagagcaagg 660

ctgggggtgc tctgtgcgcc aatggcgcgg tgaggcaagg tgacgatggc gccgccctgg 720

aggtgatcga ggtgcaccga gtgggcaact ccaaagagca cttgcctctg cccagcgagg 780

ctggtcctac cccttgtgcc 800

<210> SEQ ID NO 180
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 180

ggcacaaggg gtaggaccag cctcgctggg cagaggcaag tgctctttgg agttgcccac 60

tcggtgcacc tcgatcacct ccagggcggc gccatcgtca ccttgcctca ccgcgccatt 120

ggcgcacaga gcacccccag ccttgctctc cacgcccagc ctccagttcc tgctccccga 180

ctctccattc acactcttct tgggctgcgg ggcgggagat gctccatggc gggtgtccgc 240

tccggtcttc tccacctttt tgaccgtctt gcggatgcgg aagcgcgcag ctcggaatat 300

gcgcccatag agaaccagca tgagcagcag cgggatgtag aaagctccaa aggtggaata 360

gatagtgtag ccatgatcct tgctaatggt gcatgcgtcg gggtccgagc ggtcttccgg 420

ggtgcgccag cccagcatgg gcgggataga gatgaggaag ccaataagcc aagtgagcga 480

gatgagcgca gcggcgcgcc ggggcgtcct cttgttcacg tagtcgatgg ggtccgtgat 540

ggcccagtac ctgtccagcg cgatggcgca caggtgcaag atggatgagg tgcagcacag 600

cacgtcgagg gcgatgaaca ggtcgcaggt tacctggccc agtgtccact tgttgagcac 660

ctgatacagc gcggccatgg gcagcaccaa caccgacacc atgaggtcgg tgaccgccaa 720

agagccaata agataattgg ccacgttctg cagggagcgc tccaaggcga tggcagccac 780

cacgcacgca ttgcccagca 800

<210> SEQ ID NO 181
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 181

tgacgcaagg tccagtccag attgccaggc ccggggcatg agagaggatc cttgtaggtt 60

tcggaggtgg gggggctgca ctccattgtt cactccgggc caatcagggt tggcccactt 120

cctcccagcc aatctccctt cacccccagc ctccaaccca acccaccccg cccatcagcc 180 cctggatccc catcacctcc cccgcatccc cggcagttct ggggaagctt cgtgacgcca 240

caggtcccgc ccccagctcc ggcccggggc tagtgcgtgt tgacgtcatg ctgcgtgcgg 300

gccggtgcgg aatcgctcct tcaactccgc ggggcagtag gagttagtta gcaaagagcc 360

gaggccgggc gcgcgaccct cgtccttctg cccctggccg cacactttgc gcacatctct 420

ttttctgcat ggtggatatt atttttcatt atccttttct gggtgctatg ggtgatcatt 480

ccaagagtaa gtatttctgt gtgtgtgtgg ggtggggtgt gtgtgtatgc ttaatatgca 540

aaatttctaa 550

<210> SEQ ID NO 182
<211> LENGTH: 550
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 182

ttagaaattt tgcatattaa gcatacacac acaccccacc ccacacacac acagaaatac 60

ttactcttgg aatgatcacc catagcaccc agaaaaggat aatgaaaaat aatatccacc 120

atgcagaaaa agagatgtgc gcaaagtgtg cggccagggg cagaaggacg agggtcgcgc 180

gcccggcctc ggctctttgc taactaactc ctactgcccc gcggagttga aggagcgatt 240

ccgcaccggc ccgcacgcag catgacgtca acacgcacta gccccgggcc ggagctgggg 300

gcgggacctg tggcgtcacg aagcttcccc agaactgccg gggatgcggg ggaggtgatg 360

gggatccagg ggctgatggg cggggtgggt tgggttggag gctgggggtg aagggagatt 420

ggctgggagg aagtgggcca accctgattg gcccggagtg aacaatggag tgcagccccc 480

ccacctccga aacctacaag gatcctctct catgccccgg gcctggcaat ctggactgga 540

ccttgcgtca 550

<210> SEQ ID NO 183
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 183

cagggaacag acccagtagt tggcttggat ctcttaactc cagaaaaggc cgagtgagga 60

caagggagac cacagggata atttctgtgg ctctggtaag gggatgacaa gggagaaaaa 120

ctttcccacg gttccgtctg gcccgcggcg cttgtctgcc tgcgcggggt caaagcccgg 180

cgccgcccac gcgcggctcg ggtgggaacc cgcagacgtg gggcgagcag ggccgctggc 240

tgtggcgggc gagcgccggg gcgccacgtc cgaggccgcg gggtcggggc tgcaggcaca 300

gctcgagcgc tttccgcggg gtttggctcc tgtcgcttcc cgtctcgccg aaccggcatc 360

gccgccgccg gagccgcagc gagtcctcag agcctggctg ctggcggccg ggagcgccgg 420

gacggggcgc gaagccggag gctccgggac gtggatacag gtaaaggccg gcgggtcgga 480

gtcgggcggg gcgcggcggc ggcgcctctc ggagggacct ggcctcggcc gggccctacc 540

cagccgcggt ggcccgggcc cccacgttgg cccaggcggg gacgtgccaa ggggctgggc 600

tagggttgcc gctggcctgg ccgcctctcg cccggcgggc ctcaggtgac gcggccgcgg 660

cttaactttc gcacctgagg ctctcggagc ggcctcgggg cgcgcccacc tggaggttgg 720

aattacacag ggtcgaaaaa gctgagtcct ggaggcgagg cgctgtaggt gtggcggagg 780

aggccgggga aggtggggtg ggtgccaggg gtccagtact gaaccctctc caggtctgag 840

gtggggaact gcgtcttgtt taatttcgga gcttgtgggg accacacagc cccttccacg 900 gccgattccc tctgcacggt tccactttcc tttgtctagc ccatttcagt atcggcgtcg 960

cagtcgcttt tgttgcagcc ttgggtccgg agtgtacgac tttctgctag gcagaggtca 1020

taagctctga aatccatcgg gcggaggtgg 1050

<210> SEQ ID NO 184
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 184

ccacctccgc ccgatggatt tcagagctta tgacctctgc ctagcagaaa gtcgtacact 60

ccggacccaa ggctgcaaca aaagcgactg cgacgccgat actgaaatgg gctagacaaa 120

ggaaagtgga accgtgcaga gggaatcggc cgtggaaggg gctgtgtggt ccccacaagc 180

tccgaaatta aacaagacgc agttccccac ctcagacctg gagagggttc agtactggac 240

ccctggcacc caccccacct tccccggcct cctccgccac acctacagcg cctcgcctcc 300

aggactcagc tttttcgacc ctgtgtaatt ccaacctcca ggtgggcgcg ccccgaggcc 360

gctccgagag cctcaggtgc gaaagttaag ccgcggccgc gtcacctgag gcccgccggg 420

cgagaggcgg ccaggccagc ggcaacccta gcccagcccc ttggcacgtc cccgcctggg 480

ccaacgtggg ggcccgggcc accgcggctg ggtagggccc ggccgaggcc aggtccctcc 540

gagaggcgcc gccgccgcgc cccgcccgac tccgacccgc cggcctttac ctgtatccac 600

gtcccggagc ctccggcttc gcgccccgtc ccggcgctcc cggccgccag cagccaggct 660

ctgaggactc gctgcggctc cggcggcggc gatgccggtt cggcgagacg ggaagcgaca 720

ggagccaaac cccgcggaaa gcgctcgagc tgtgcctgca gccccgaccc cgcggcctcg 780

gacgtggcgc cccggcgctc gcccgccaca gccagcggcc ctgctcgccc cacgtctgcg 840

ggttcccacc cgagccgcgc gtgggcggcg ccgggctttg accccgcgca ggcagacaag 900

cgccgcgggc cagacggaac cgtgggaaag tttttctccc ttgtcatccc cttaccagag 960

ccacagaaat tatccctgtg gtctcccttg tcctcactcg gccttttctg gagttaagag 1020

atccaagcca actactgggt ctgttccctg 1050

<210> SEQ ID NO 185
<211> LENGTH: 1800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 185

ggcagcagcc gctggcttct gcgcccacta ggagcttcgg atgcccgagt tagggctgcg 60

ccaaggcggc cggagcagag agggagacgg ggacggggac aggcagggac aaagtgcaag 120

aggcaaaact ggctgaaaag cagaagtgta ggagccgcca aggggcggga cgaacaggtc 180

cgtgggccgg gcggagccaa gggtgggggc cggggtccct ccaggtggca ctcgcggcgc 240

tagtccccag cctcctccct tcccccggcc ctgattggca ggcggcctgc gaccagccgc 300

gaacgccaca gcgccccggg cgcccaggag aacgcgaacg gccccccgcg ggagcgggcg 360

agtaggaggg ggcgccgggc tatatatata gcggctcggc ctcgggcggg cctggcgctc 420

agggaggcgc gcactgctcc tcagagtccc agctccagcc gcgcgctttc cgcccggctc 480

gccgctccat gcagccgggg tagagcccgg cgcccggggg ccccgtcgct tgcctcccgc 540

acctcctcgg ttgcgcactc ctgcccgagg tcggccgtgc gctcccgcgg gacgccacag 600

gcgcagctct gccccccagc ttcccgggcg cactgaccgc ctgaccgacg cacggccctc 660 gggccgggat gtcggggccc gggacggccg cggtagcgct gctcccggcg gtcctgctgg 720

ccttgctggc gccctgggcg ggccgagggg gcgccgccgc acccactgca cccaacggca 780

cgctggaggc cgagctggag cgccgctggg agagcctggt ggcgctctcg ttggcgcgcc 840

tgccggtggc agcgcagccc aaggaggcgg ccgtccagag cggcgccggc gactacctgc 900

tgggcatcaa gcggctgcgg cggctctact gcaacgtggg catcggcttc cacctccagg 960

cgctccccga cggccgcatc ggcggcgcgc acgcggacac ccgcgacagt gagtggcgcg 1020

gccaggcgcg aaggggcggg ggcgggggc aacggccgcc gggccaaccc gctcagtcac 1080

actctgagac cctcggcggg cacctgctcg ggggccccgg gaaccggggc ggactcgggc 1140

tccggtccct tctgacgcgg ggctggggac gcagacactc ttggctccgg cagcccagcg 1200

caacccctga ggtcgggcgc cgcctcccgc cttcagaaac tcgggctccg agcgccgaat 1260

tccagcgcct tcgcccgtgg gcacagggcg cgcggtgcag ccacaggggg cccgagacac 1320

gcgccccggc ctggcccagg ctggggaacc gctggggtcg ggctcgcgtc tgaaggtccg 1380

ggactgggtg cggccgccgg gggtccccta cacaggcaag ctaatctgag ctagcgcagg 1440

cttgggctcc ggaggcccta gagggcagct tgggctctgg aggcccttgg gggcggctgc 1500

gccgggaacc ctggcccttt atccccaacc ccaccccaga aatagggtcc ccggaggcga 1560

acaagccgag gggcggagtg ggccagggat cacctgcccc gcaatgacct gcgccccgcc 1620

cccaggcctg ctggagctct cgcccgtgga gcggggcgtg gtgagcatct tcggcgtggc 1680

cagccggttc ttcgtggcca tgagcagcaa gggcaagctc tatggctcgg tgagtaccgc 1740

aggggtctgg ctaggcacct agttgggaac agcggacatg gctagcaggc tcgtggcttc 1800

<210> SEQ ID NO 186
<211> LENGTH: 1800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 186

gaagccacga gcctgctagc catgtccgct gttcccaact aggtgcctag ccagacccct 60

gcggtactca ccgagccata gagcttgccc ttgctgctca tggccacgaa gaaccggctg 120

gccacgccga agatgctcac cacgccccgc tccacgggcg agagctccag caggcctggg 180

ggcggggcgc aggtcattgc ggggcaggtg atccctggcc cactccgccc ctcggcttgt 240

tcgcctccgg ggaccctatt tctggggtgg ggttggggat aaagggccag ggttcccggc 300

gcagccgccc ccaagggcct ccagagccca agctgccctc tagggcctcc ggagcccaag 360

cctgcgctag ctcagattag cttgcctgtg taggggaccc ccggcggccg cacccagtcc 420

cggaccttca gacgcgagcc cgaccccagc ggttccccag cctgggccag gccggggcgc 480

gtgtctcggg ccccctgtgg ctgcaccgcg cgccctgtgc ccacgggcga aggcgctgga 540

attcggcgct cggagcccga gtttctgaag gcgggaggcg gcgcccgacc tcaggggttg 600

cgctgggctg ccggagccaa gagtgtctgc gtccccagcc ccgcgtcaga agggaccgga 660

gcccgagtcc gccccggttc ccggggcccc cgagcaggtg cccgccgagg gtctcagagt 720

gtgactgagc gggttggccc ggcggccgtt gcccccgcc cccgcccctt cgcgcctggc 780

cgcgccactc actgtcgcgg gtgtccgcgt gcgcgccgcc gatgcggccg tcggggagcg 840

cctggaggtg gaagccgatg cccacgttgc agtagagccg ccgcagccgc ttgatgccca 900

gcaggtagtc gccggcgccg ctctggacgg ccgcctcctt gggctgcgct gccaccggca 960

ggcgcgccaa cgagagcgcc accaggctct cccagcggcg ctccagctcg gcctccagcg 1020 tgccgttggg tgcagtgggt gcggcggcgc cccctcggcc cgcccagggc gccagcaagg 1080

ccagcaggac cgccgggagc agcgctaccg cggccgtccc gggccccgac atcccggccc 1140

gagggccgtg cgtcggtcag gcggtcagtg cgcccgggaa gctgggggc agagctgcgc 1200

ctgtggcgtc ccgcgggagc gcacggccga cctcgggcag gagtgcgcaa ccgaggaggt 1260

gcgggaggca agcgacgggg cccccgggcg ccgggctcta ccccggctgc atggagcggc 1320

gagccgggcg gaaagcgcgc ggctggagct gggactctga ggagcagtgc gcgcctccct 1380

gagcgccagg cccgcccgag gccgagccgc tatatatata gcccggcgcc ccctcctact 1440

cgcccgctcc cgcggggggc cgttcgcgtt ctcctgggcg cccggggcgc tgtggcgttc 1500

gcggctggtc gcaggccgcc tgccaatcag ggccgggga agggaggagg ctggggacta 1560

gcgccgcgag tgccacctgg agggaccccg gcccccaccc ttggctccgc ccggcccacg 1620

gacctgttcg tcccgcccct tggcggctcc tacacttctg cttttcagcc agttttgcct 1680

cttgcacttt gtccctgcct gtccccgtcc ccgtctccct ctctgctccg gccgccttgg 1740

cgcagcccta actcgggcat ccgaagctcc tagtgggcgc agaagccagc ggctgctgcc 1800

<210> SEQ ID NO 187
<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 187

tgaggtgagg ggccggagga gcaagggaca agaggagcag aggacaggtg atggaaatcc 60

tgcagcttta ggctccattc tgccatctac atcccagcgc agggtgaagc ctgagagccc 120

aaatggccaa ctccacaggg ctgaacgcct cagaagtcgc aggctcgttg ggttgatcc 180

tggcagctgt cgtggaggtg gggcactgc tgggcaacgg cgcgctgctg gtcgtggtgc 240

tgcgcacgcc gggactgcgc gacgcgctct acctggcgca cctgtgcgtc gtggacctgc 300

tggcggccgc ctccatcatg ccgctgggcc tgctggccgc accgccgccc gggctgggcc 360

gcgtgcgcct gggccccgcg ccatgccgcg ccgctcgctt cctctccgcc gctctgctgc 420

cggcctgcac gctcggggtg gccgcacttg gcctggcacg ctaccgcctc atcgtgcacc 480

cgctgcggcc aggctcgcgg ccgccgcctg tgctcgtgct caccgccgtg tgggccgcgg 540

cgggactgct gggcgcgctc tccctgctcg gcacgccgcc cgcaccgccc cctgctcctg 600

ctcgctgctc ggtcctggct gggggcctcg ggcccttccg gccgctctgg gccctgctgg 660

ccttcgcgct gcccgccctc ctgctgctcg gcgcctacgg cggcatcttc gtggtggcgc 720

gtcgcgctgc cctgaggccc ccacggccgg cgcgcgggtc ccgactccac tcggactctc 780

tggatagccg cctttccatc ttgccgccgc tccggcctcg cctgcccggg ggcaaggcgg 840

ccctggcccc agcgctggcc gtgggccaat ttgcagcctg ctggctgcct tatggctgcg 900

cgtgcctggc gcccgcagcg cgggccgcgg aagccgaagc ggctgtcacc tgggtcgcct 960

actcggcctt cgcggctcac cccttcctgt acgggctgct gcagcgcccc gtgcgcttgg 1020

cactgggccg cctctctcgc cgtgcactgc ctggacctgt gcgggcctgc actccgcaag 1080

cctggcaccc gcgggcactc ttgcaatgcc tccagagacc cccagagggc cctgccgtag 1140

gcccttctga ggctccagaa cagaccccg agttggcagg agggcggagc cccgcatacc 1200

aggggccacc tgagagttct ctctcctgag caggagaaag gagggtggtt tccgtggggg 1260

ctcatccaac ccctgcacag gtcacagcag gtgccctgct 1300

<210> SEQ ID NO 188

<211> LENGTH: 1300
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 188

agcagggcac ctgctgtgac ctgtgcaggg gttggatgag cccccacgga aaccaccctc 60

ctttctcctg ctcaggagag agaactctca ggtggcccct ggtatgcggg gctccgccct 120

cctgccaact cgggggtctg ttctggagcc tcagaagggc ctacggcagg gccctctggg 180

ggtctctgga ggcattgcaa gagtgcccgc gggtgccagg cttgcggagt gcaggcccgc 240

acaggtccag gcagtgcacg gcgagagagg cggcccagtg ccaagcgcac ggggcgctgc 300

agcagcccgt acaggaaggg gtgagccgcg aaggccgagt aggcgaccca ggtgacagcc 360

gcttcggctt ccgcggcccg cgctgcgggc gccaggcacg cgcagccata aggcagccag 420

caggctgcaa attggcccac ggccagcgct ggggccaggg ccgccttgcc cccgggcagg 480

cgaggccgga gcggcggcaa gatggaaagg cggctatcca gagagtccga gtggagtcgg 540

gacccgcgcg ccggccgtgg gggcctcagg gcagcgcgac gcgccaccac gaagatgccg 600

ccgtaggcgc cgagcagcag gagggcgggc agcgcgaagg ccagcagggc ccagagcggc 660

cggaagggcc cgaggccccc agccaggacc gagcagcgag caggagcagg gggcggtgcg 720

ggcggcgtgc cgagcaggga gagcgcgccc agcagtcccg ccgcggccca cacggcggtg 780

agcacgagca caggcggcgg ccgcgagcct ggccgcagcg ggtgcacgat gaggcggtag 840

cgtgccaggc caagtgcggc caccccgagc gtgcaggccg gcagcagagc ggcggagagg 900

aagcgagcgg cgcggcatgg cgcggggccc aggcgcacgc ggcccagccc gggcggcggt 960

gcggccagca ggcccagcgg catgatggag gcggccgcca gcaggtccac gacgcacagg 1020

tgcgccaggt agagcgcgtc gcgcagtccc ggcgtgcgca gcaccacgac cagcagcgcg 1080

ccgttgccca gcagtgcccc cacctccacg acagctgcca ggatcaaccc caacgagcct 1140

gcgacttctg aggcgttcag ccctgtggag ttggccattt gggctctcag gcttcaccct 1200

gcgctgggat gtagatggca gaatggagcc taaagctgca ggatttccat cacctgtcct 1260

ctgctcctct tgtcccttgc tcctccggcc cctcacctca 1300

<210> SEQ ID NO 189
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 189

ccgcgacctt cgagaacccg catgctgttc tccaccaggt ctctcagtcc tccctgcccc 60

aatccccatg cccgcctccg cgaccctgtg atgcctccct tcttgcacag gagcagtgac 120

ctcagcactt acttaatcct ctcccggcgc cgagctcagt tggagaggct aggggtggta 180

gtgactggca ggaggccggg gcggggggaa cccccaagcc cggcgtctgg ggctgcgggt 240

ccgacccgag atccgccctc cctgcaagcc ccgagccgct ggccaggccc gctactgcgc 300

accagccgca tccgcgagcg ctggctctgc cggcctgagc tagggtgggt agggccggga 360

cccacggcgg aggtggggcc gggccgagca gcctcggggg atccccgaag ctacagcgcc 420

ttgcctccct gcacgctccg cgcccccggc ctccgattgg ctgtcgggcc tagagcccgc 480

ccagaattgg accgttcgct tgtcgctcgg gtctggctcc acccccagag ggagcctaga 540

acctggtcgc agtttttaga gactaccctc accccgtggc ctgcgccgaa gttgggcgga 600

ggacagtggg tggccaggcc cttccgggcc agaactcggg acccctgcca gctacccgtg 660

-continued

ccaggacaga ctcaagcccc caaaacgcgg atggatgtac agaggagact tggggagagc 720

actggactgg gagtccttgg gcctgcactg aactctggct gactttgtga ccttgaagaa 780

actgcttttc ccttcctgaa 800

<210> SEQ ID NO 190
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 190

ttcaggaagg gaaaagcagt ttcttcaagg tcacaaagtc agccagagtt cagtgcaggc 60

ccaaggactc ccagtccagt gctctcccca agtctcctct gtacatccat ccgcgttttg 120

ggggcttgag tctgtcctgg cacgggtagc tggcaggggt cccgagttct ggcccggaag 180

ggcctggcca cccactgtcc tccgcccaac ttcggcgcag gccacggggt gagggtagtc 240

tctaaaaact gcgaccaggt tctaggctcc ctctgggggt ggagccagac ccgagcgaca 300

agcgaacggt ccaattctgg gcgggctcta ggcccgacag ccaatcggag gccgggggcg 360

cggagcgtgc agggaggcaa ggcgctgtag cttcggggat cccccgaggc tgctcggccc 420

ggccccacct ccgccgtggg tcccggccct acccacccta gctcaggccg gcagagccag 480

cgctcgcgga tgcggctggt gcgcagtagc gggcctggcc agcggctcgg ggcttgcagg 540

gagggcggat ctcgggtcgg acccgcagcc ccagacgccg ggcttggggg ttcccccgc 600

cccggcctcc tgccagtcac taccacccct agcctctcca actgagctcg gcgccgggag 660

aggattaagt aagtgctgag gtcactgctc ctgtgcaaga agggaggcat cacagggtcg 720

cggaggcggg catggggatt ggggcaggga ggactgagag acctggtgga gaacagcatg 780

cgggttctcg aaggtcgcgg 800

<210> SEQ ID NO 191
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 191

ctgcagcagg acgtaagcac agtcatcgct gcaaactgca aactcgtaag cacagtcatc 60

gctgcaaact gcaaactcgt gctccgagcg ctgccctccc ctgtggagcg gaggaggga 120

ggcctggggc cgcggcggtg tgcgccccgc tctgaccgca gagcccctt cccgaggaaa 180

gcggctggcc cggtcccggc tggtgatcac gcggggcccc tgtctgcttg gtgcgcaggt 240

gagggtctgc ccttccgctg cgccccggac agcctggagg tgagcacgcg ctgggccctg 300

gaccgcgagc agcgggagaa gtacgagctg gtggccgtgt gcaccgtgca cgccggcgcg 360

cgcgaggagg tggtgatggt gcccttcccg gtgaccgtgt acgacgagga cgactcggcg 420

cccaccttcc ccgcgggcgt cgacaccgcc agcgccgtgg tggagttcaa gcggaaggag 480

gtgcttgtcc gcgcgtgctg tggtctaccc agtgtctgtc tccggccaca gttcgtttct 540

cggtcggttt agtgtccgtg tagccaccca accgtgtggc cgaccattcg cgctttcatt 600

tgtccttcgc ctccgtctgc gccgtctgtc ctagggggag gggaaggggg agtcctgcca 660

gcacccagct gggccttgcc tcgggaggca aggaccagga cgaggcccga gggctcgcgt 720

ctggggcata cttgtgccgc tgcaggcggg cgcggcgcgc tgcccgggcg gggagcatct 780

gccgggaggg cactccctcc caccagcagt tagcccccaa cgggagggcc cttgagtgac 840

cacgagcaga gccggggatt ggagaaggac gggaaggcgg atcacctccg gcgccgcccg 900

-continued

ccccgccctt ctccggctcg cgctggtgga gcgcgaccgc cacctgctgg gcctcggcct 960

tcctgcagcc ggcccaccca gcaggggccg tgggagagtg ggcgtgggga ctgaggtagg 1020

tagtacgttg ccttgttccg cttctctggg 1050

<210> SEQ ID NO 192
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 192

cccagagaag cggaacaagg caacgtacta cctacctcag tccccacgcc cactctccca 60

cggcccctgc tgggtgggcc ggctgcagga aggccgaggc ccagcaggtg gcggtcgcgc 120

tccaccagcg cgagccggag aagggcgggg cgggcggcgc cggaggtgat ccgccttccc 180

gtccttctcc aatccccggc tctgctcgtg gtcactcaag ggccctcccg ttgggggcta 240

actgctggtg ggagggagtg ccctcccggc agatgctccc cgcccgggca gcgcgccgcg 300

cccgcctgca gcggcacaag tatgccccag acgcgagccc tcgggcctcg tcctggtcct 360

tgcctcccga ggcaaggccc agctgggtgc tggcaggact ccccccttccc ctccccctag 420

gacagacggc gcagacggag gcgaaggaca aatgaaagcg cgaatggtcg gccacacggt 480

tgggtggcta cacggacact aaaccgaccg agaaacgaac tgtggccgga gacagacact 540

gggtagacca cagcacgcgc ggacaagcac ctccttccgc ttgaactcca ccacggcgct 600

ggcggtgtcg acgcccgcgg ggaaggtggg cgccgagtcg tcctcgtcgt acacggtcac 660

cgggaagggc accatcacca cctcctcgcg cgcgccggcg tgcacggtgc acacggccac 720

cagctcgtac ttctcccgct gctcgcggtc cagggcccag cgcgtgctca cctccaggct 780

gtccggggcg cagcggaagg gcagaccctc acctgcgcac caagcagaca ggggccccgc 840

gtgatcacca gccgggaccg ggccagccgc tttcctcggg aagggggctc tgcggtcaga 900

gcggggcgca caccgccgcg gccccaggcc tcccctcctc cgctccacag gggagggcag 960

cgctcggagc acgagtttgc agtttgcagc gatgactgtg cttacgagtt tgcagtttgc 1020

agcgatgact gtgcttacgt cctgctgcag 1050

<210> SEQ ID NO 193
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 193

gcgccgacgg gggcgggtgg taggggatgt acgggtgtgt atatgcagag gtatgccagg 60

ctctgcccct taaagtttgg gggccggcgg aggcggcgcc gtggccggga gaaagtgtct 120

ctcatttagg agggtttgca ggtccagagt aaagtcactg aagagtggaa gcgaggaagg 180

aacaggatga ttagacctca gctgcggacc gcggggctgg gacgatgcct cctgccgggg 240

ctgctgctgc tcctggtgcc cgtcctctgg gccggggctg aaaagctaca tacccagccc 300

tcctgccccg cggtctgcca gcccacgcgc tgccccgcgc tgcccacctg cgcgctgggg 360

accacgccgg tgttcgacct gtgccgctgt tgccgcgtct gccccgcggc cgagcgtgaa 420

gtctgcggcg gggcgcaggg ccaaccgtgc gccccggggc tgcagtgcct ccagccgctg 480

cgccccgggt tccccagcac ctgcggttgc ccgacgctgg gaggggccgt gtgcggcagc 540

gacaggcgca cctaccccag catgtgcgcg ctccgggccg aaaaccgcgc cgcgcgccgc 600

ctgggcaagg tcccggccgt gcctgtgcag tgggggaact gcggggatac aggtgagccg 660 cgggggcgcg cgccctcgga acactttcta actctggagg agcgtaaagg aacaagacct 720

cactgagacc gcacagttcg cgcctggtcc tcctgcgtca tttgcctcct ggattcgaca 780

cctctgtgtt cctgatttcc 800

<210> SEQ ID NO 194
<211> LENGTH: 800
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 194

ggaaatcagg aacacagagg tgtcgaatcc aggaggcaaa tgacgcagga ggaccaggcg 60

cgaactgtgc ggtctcagtg aggtcttgtt cctttacgct cctccagagt tagaaagtgt 120

tccgagggcg cgcgcccccg cggctcacct gtatccccgc agttccccca ctgcacaggc 180

acggccggga ccttgcccag gcggcgcgcg gcgcggtttt cggcccggag cgcgcacatg 240

ctggggtagg tgcgcctgtc gctgccgcac acggcccctc ccagcgtcgg gcaaccgcag 300

gtgctgggga acccggggcg cagcggctgg aggcactgca gccccggggc gcacggttgg 360

ccctgcgccc cgccgcagac ttcacgctcg gccgcggggc agacgcggca acagcggcac 420

aggtcgaaca ccggcgtggt ccccagcgcg caggtgggca gcgcggggca gcgcgtgggc 480

tggcagaccg cggggcagga gggctgggta tgtagctttt cagccccggc ccagaggacg 540

ggcaccagga gcagcagcag ccccggcagg aggcatcgtc ccagccccgc ggtccgcagc 600

tgaggtctaa tcatcctgtt ccttcctcgc ttccactctt cagtgacttt actctggacc 660

tgcaaaccct cctaaatgag agacactttc tcccggccac ggcgccgcct ccgccggccc 720

ccaaacttta aggggcagag cctggcatac ctctgcatat acacacccgt acatccccta 780

ccacccgccc ccgtcggcgc 800

<210> SEQ ID NO 195
<211> LENGTH: 801
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 195

ttgtcttctc ccttccgacc tcccgtggcc ccagcgcggc cagctcacag taggtgctcg 60

ggcagcgttt cttcagggac ctagacggcc tggagaggaa gggccccagc ccagccgccc 120

gggcctctca cctggctctc ggggcgcccg gctcgcactt cctcccgccg ccccgcccct 180

tccacattcc tgccccgccg ggcctgcccc gcgcagtctg ggtctctgcg ccgcagccgc 240

ccgcccgccc gctcagcgcc cggccccggg atgacggcgg cccaggccgc gggtgaggag 300

gcgccaccag gcgtgcggtc cgtcaaggtg gtcctggtgg gcgacggcgg ctgcgggaag 360

acgtcgctgc tgatggtctt cgccgatggg gccttccccg aggtgagtgc cccgcgcctc 420

cgcctcgccc ggttccgctc gcgcgcccgg gtgtacaggt ccgtgccgga gcggcccagg 480

ctgtgcgcct aacccggcct ccgaggggtg tcccagcggg gcctggggtc cagggcagag 540

ttcttccgcc ccagccattg ggaatgaagg cctcagtgat gttatctgta aagccggagg 600

aatggcatcc accggggaga ggtgtcacaa ggactgagtg aggcgacctg ggtgcacaca 660

agatcctaag acagcacttg gccacacaat tccgctgagg gcctgagagc ttggaagcca 720

gactgccgag gttcaaatta tggctttgcc tcttatagct gtgtgccctt gggtaagtcc 780

cctaaccctg ctgtgcctgt g 801

<210> SEQ ID NO 196

<211> LENGTH: 1301
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 196

attgagagag agggagggcg aaaggaagga aggggagcca gaggtgggag tggaagaggc 60

agcctcgcct ggggctgatt ggctcccgag gccagggctc tccaagcggt ttataagagt 120

tggggctgcc gggcgccctg cccgctcgcc cgcgcgcccc aggacccaaa gccgggctcc 180

aagtcggcgc cccacgtcga ggctccgccg cagcctccgg agttggccgc agacaagaag 240

gggagggagc gggagaggga ggagagctcc gaagcgagag ggccgagcgc catgcgccgc 300

gccagcagag actacaccaa gtacctgcgt ggctcggagg agatgggcgg cggccccgga 360

gccccgcacg agggccccct gcacgccccg ccgccgcctg cgccgcacca gccccctgcc 420

gcctcccgct ccatgttcgt ggccctcctg ggctggggc tgggccaggt tgtctgcagc 480

gtcgccctgt tcttctattt cagagcgcag gtgagtggcc accttcccag gggatcgcgg 540

ctgagagcgc ccatctcctt cccccgcact tggaaactga gtctggcggc agggctgggc 600

cacccagagc ttgcatattc cggaagggaa agtgactcca gaagggagag aggaagtgtt 660

gagtttgggg acaacctggc gcagggctgt cgggcgcacc ctgctctctc tccgcccacg 720

caccccagct tctcggtgct ctgggggcgg actcccctgg ccggacgatg ggtttgaatc 780

tcaccccgtc ccttcgctgg gaaacaacac tggcctctca ccttttctgg tagtgattgc 840

atactttttc tccctgtcat ttctcacttg aagttaagaa tcaacttctg ttcacgtagg 900

aaaaaagatg agcgccttca cttgggcatc tacctttccc ttcccgccca ccacccggcg 960

ggtttcggtt cctgcgcctg gctgctctgc aggtgtgctg gggccacggt gctggagggc 1020

tgcgcggagc gggaggtcgc ggtgctcgtg cccaggtcgc ccaatgggtg ggcagaatga 1080

cacggcgcga ccagagaggc gcgggctcgg gatgggggct ctgcggctgt ggcgctgtcc 1140

tgtgggggtg aaggaagagg gacagcccca cgtgcctgct agggatgtgg gcggaggaag 1200

gaagcgaggt gagtgtgatg gcacagtgtt actacagtct agcaaataac caaccttcgg 1260

aaagatgaag aggtttttg cacgacggct aggaactgca g 1301

<210> SEQ ID NO 197
<211> LENGTH: 4301
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 197

gcaatttata gatgagagcg tggacggcag agagcattgt gtatgttgaa gtctctgcga 60

tatggggtgt ccctgctgcc ccgctccagc ctttcacttc tgacctcctt cctctggctc 120

ttacgctaca ggatccaaaa ctactcggaa gacttgccgc gggcggtgat tgacgacgcc 180

tttgcccgcg ccttcgcact gtggagcgcg gtgacgccgc tcaccttcac tcgcgtgtac 240

agccgggacg cagacatcgt catccagttt ggtgtcgcgg gtgagaacgt gaggagggaa 300

aatccaagag acctgggcgg ggtcagggaa gggaggacca cggagagcgt ggaggcagca 360

gtggccccgg cttcctcttg cctgcccgcg ctgccctggc ttatacggcc cctcctgcca 420

gacagtgcac agggccaggg cgccaggctg ggagagcttc gcgcaggcgg gatttcagcc 480

cgcacttatt tcggagccct tgccttgggc agcgcacaat ctgcgcagca gtactcggct 540

aaccctcttc ctctcgacct gtttcttcag agcacggaga cgggtatccc ttcgacggga 600

aggacgggct cctggcacac gcctttcctc ctggccccgg cattcaggga gacgcccatt 660

-continued

```
tcgacgatga cgagttgtgg tccctgggca agggcgtcgg tgagattctg agtcctcctg    720

gcccctgatt cccttcattc tctcccactc atcacccgcc gccctaactc cggtcccccc    780

tcctcctgca gtggttccaa ctcggtttgg aaacgcagat ggcgcggcct gccacttccc    840

cttcatcttc gagggccgct cctactctgc ctgcaccacc gacggtcgct ccgacggctt    900

gccctggtgc agtaccacgg ccaactacga caccgacgac cggtttggct tctgccccag    960

cgagagtgag tgaggggct cgccgagggc tgggggcgcc caccaccctt gatggtcctg   1020

ggttctaatt ccagctctgc cactagtgct gtgtggcctg caattcaccc tcccgcactc   1080

tgggcccaat tttctcatct gagaaatgat gagagatggg atgaactgca gaccatccat   1140

gggtcaaaga acaggacaca cttgggggtt ataatgtgct gtctccgcct tctccccctt   1200

tcccacatcc tcctcgcccc aggactctac acccaggacg gcaatgctga tgggaaaccc   1260

tgccagtttc cattcatctt ccaaggccaa tcctactccg cctgcaccac ggacggtcgc   1320

tccgacggct accgctggtg cgccaccacc gccaactacg accgggacaa gctcttcggc   1380

ttctgcccga cccgaggtac ctccaccctg tctaccaggt tcagccccgc cctctcatca   1440

tgtattggcc cccaaaacgc ggctcttccc tcccatcagt ttgtctttcc actctcattg   1500

gtcctcagga cgaccgtgac tccgcccacc tacaccacat ttccaccact atccctgact   1560

tccaatggcc ccgccccagc cactaaggtt cggccttttc tgcccagctg gccgcctctt   1620

ccttggtctg gtgtcccagg caccgcccac gggtctagcc tcttctcagg agtgctctac   1680

agcgccccct aggccaccaa gattgtttag ctccctgtcg ggtcggcccc tgactcctta   1740

ttggactcat ccatctggct catccaaggc cttgggtctc tccagctgac tcgacggtga   1800

tggggggcaa ctcggcgggg gagctgtgcg tcttcccctt cactttcctg ggtaaggagt   1860

actcgacctg taccagcgag ggccgcggag atgggcgcct ctggtgcgct accacctcga   1920

actttgacag cgacaagaag tggggcttct gcccggacca aggtaggcgt ggtcccgcgg   1980

ctccggggct ggggttcccg gcagtggtgg tggtggggtg gccagggctg ggggctcggc   2040

ccggcgctca cgtctcaggc tccctctccc tccaggatac agtttgttcc tcgtggcggc   2100

gcatgagttc ggccacgcgc tgggcttaga tcattcctca gtgccggagg cgctcatgta   2160

ccctatgtac cgcttcactg aggggccccc cttgcataag gacgacgtga atggcatccg   2220

gcacctctat ggtgaggcag gggcagggat gggaggagga ggggaaaggg cgtggctgtg   2280

ccacagtacc aaagaattgg gggttgggga tcgggggagg aacggggcgt gcaggagagg   2340

tgggacctca acgtctgtct ggaagcagag cctgggccca gtcgctgcca tgtcagtgct   2400

tagaggtggt gataaagaga ctctagagag agataggtgt gacttcaaaa gccagtctac   2460

tctgggcatg gtggctcacg cctctaatcc cagggctttg ggagacccaa ggcgggagga   2520

ttgcttaagc ccaggagttc cagaccagcc tcggcaacat agccagactc ccatctctac   2580

aaaaaataaa tgagcaaggc gtgaaggcac atgtctgtag tcctagctac tctggaggct   2640

gaggtgggag gatctcttga gcccaggagt tcgaggctgt agtgagctat gattgcacca   2700

ctgcattcca tcctgggcca tagaggatgt cgcttaaaac gaaaaagaag aagaagaaag   2760

tcctgtggtt tgggaaggga ggctgagtga ggaggggcct gtgtgccaga ggaggcttca   2820

ctgagaagct taggggagca gatgttctag ggtacagag gtatgcagga ataggaagag   2880

tctcaccccg tgtctctttt taggtcctcg ccctgaacct gagccacggc ctccaaccac   2940

caccacaccg cagcccacgg ctcccccgac ggtctgcccc accggacccc ccactgtcca   3000

cccctcagag cgccccacag ctggccccac aggtcccccc tcagctggcc ccacaggtcc   3060
```

-continued

ccccactgct ggcccttcta cggccactac tgtgcctttg agtccggtgg acgatgcctg 3120

caacgtgaac atcttcgacg ccatcgcgga gattgggaac cagctgtatt tgttcaagga 3180

tgggtgagga ggcggggttg tgtggatgcg ggagggggct ttgcggaggg gctgcccgtc 3240

ccttcccgcc cactggccct gtgtccaagg cttagagccc gtcctttccc tcctcgcttt 3300

ctcaggaagt actggcgatt ctctgagggc agggggagcc ggccgcaggg ccccttcctt 3360

atcgccgaca agtggcccgc gctgccccgc aagctggact cggtctttga ggagcggctc 3420

tccaagaagc ttttcttctt ctctggttag ttacctactt tccctccccc gcccggtcaa 3480

tccccatcag tcaaggaggc tcaagagacc atcgataacc cacgaaacgt cttgtgcgtt 3540

ttagaaaaat acgcccccctg gcggacgcag tttagcaaac gtagggggcgg ctgagtttct 3600

gccccctcct ctccacgccc tcgcgtcgct ctacccagcg cctctgcccc tgggttgcag 3660

ggactgcggg cacgcgggct aggaaaggcc tcgccggaat ctccctcctc gcgttctagg 3720

agtacgtgct ccctctgcgc ccccaaaccg acgtgaccct cctcccctgc agggcgccag 3780

gtgtgggtgt acacaggcgc gtcggtgctg ggcccgaggc gtctggacaa gctgggcctg 3840

ggagccgacg tggcccaggt gaccggggcc ctccggagtg gcagggggaa gatgctgctg 3900

ttcagcgggc ggcgcctctg gaggtgagcg ccgccgcggc cgccggcagg gggagcccgg 3960

gcgccgtcgg tccgtccgct agccggctca gcacctgtct cctccgcgcc tgcccgcagg 4020

ttcgacgtga aggcgcagat ggtggatccc cggagcgcca gcgaggtgga ccggatgttc 4080

cccggggtgc ctttggacac gcacgacgtc ttccagtacc gaggtgaggg ctgaggagga 4140

tcccttcgtg agacaccaca ctaagctcct cttagtgagt ggtcaaattc tgagcgagga 4200

agaaaaagcc cttggaaatg gaaacaaatg ccccagcaca gacaagatcc cagcagaggc 4260

agaggccttc tccaggtcat ttaggaagtc agggatgcaa c 4301

<210> SEQ ID NO 198
<211> LENGTH: 801
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 198

caggaacttt cgagatgagg tgcctttccc aaggtgacac taagtggagg agcccagcca 60

gagtccaggg gtccttacac aaccttcggt ggtctctctt tacctgtgaa gctgcagcct 120

gcttcccagc tcgggggcgt gtacaggaga ctggacctgg ggcagcctca gaatgcctgg 180

ctgcctggag ctctcctcgc gtgtccaggc ggcctgcttg gtctccctcc tctcccctct 240

taggtgccgg ggcgggcacc cggtgcaggg tgggcacggc gcctgccacc agcctcaggc 300

gctgggagaa gcgcaggttc ttctggataa ccgaagagac gtcaaaacag gctggggcaa 360

agtggtcaga gcagatgacc gagcggtcat tgcctccgta ccagtcggcg cggcaacccc 420

gcacgaagcg gtcccagagc agccgcacgg cccggtcctt gggaaagcgg aacagcgact 480

tcccagactt ggtggtgttg ccgcagtggg cggccacaca acgggccggc atggcggccg 540

tcttcggtgc gcgggagccg ggttccctgg accttcgccc ttgggcacgc tcctcgcagc 600

ggcctcggcg aggcaagtcc tcccctcctc acctgtccac tccgggtcgg gattgtttcc 660

ttccctacct ctggtcaccg gaagtggcga tctggggccc ccaatgggag ggctctttga 720

tatcttcctc ctcctcctcc ctgcgctgct ccccaggagc cagtggacac aagcagaggg 780

atacaaattt cgcgcgggca g 801

<210> SEQ ID NO 199

```
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 199

tgatggtcgt attgcgggtt tatc                                              24


<210> SEQ ID NO 200
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 200

atacctaaac ccaacgccga ctac                                              24


<210> SEQ ID NO 201
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 201

cgcgatttga gtagttagcg tcgt                                              24


<210> SEQ ID NO 202
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 202

aaccaacgcg acgacctaac taac                                              24


<210> SEQ ID NO 203
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 203

tagatttcgg tgtttcgggc gtt                                               23


<210> SEQ ID NO 204
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 204

ccgctaattc ccaatcgtac tactca                                            26


<210> SEQ ID NO 205
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 205
```

```
ttcgtttcgt tcggtcgtga tt                                              22


<210> SEQ ID NO 206
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 206

gactacgaac gcttcgaatt cctc                                            24


<210> SEQ ID NO 207
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 207

gttgcgttgg tagcgattcg ttgt                                            24


<210> SEQ ID NO 208
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 208

cccgaaccga atcctcgaaa tct                                             23


<210> SEQ ID NO 209
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 209

gacgtagtat gatgcgcgta gtgtg                                           25


<210> SEQ ID NO 210
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 210

gcgaacatac taaacccgaa ccc                                             23


<210> SEQ ID NO 211
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 211

ggattacgtc ggtgttcgat ttgt                                            24


<210> SEQ ID NO 212
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
```

```
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 212

aacgcacgat taaccctacg cc                                              22


<210> SEQ ID NO 213
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 213

tcggattaag gtaggcgtgg tttc                                            24


<210> SEQ ID NO 214
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 214

aacgtaaacg ccgaaccgaa c                                               21


<210> SEQ ID NO 215
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 215

ggaagacgtc gttgttgatg gttt                                            24


<210> SEQ ID NO 216
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 216

accgctccga cacgaaccta tac                                             23


<210> SEQ ID NO 217
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 217

agcgttatgc gtcgcgttag tag                                             23


<210> SEQ ID NO 218
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 218

gcaaacgacg acgaaacgta ca                                              22


<210> SEQ ID NO 219
```

```
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 219

gaagagagcg ggttcgggat aag                                            23


<210> SEQ ID NO 220
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 220

ctacaacatc gtaaacgcgc gac                                            23


<210> SEQ ID NO 221
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 221

gagaagagga aggtagaagg ag                                             22


<210> SEQ ID NO 222
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 222

ctacctaact ataaccaacc c                                              21


<210> SEQ ID NO 223
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 223

acggaggagg atagtagtac g                                              21


<210> SEQ ID NO 224
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (6)..(6)
<223> OTHER INFORMATION: "y" may be "c" or "t"

<400> SEQUENCE: 224

aggtaygttg tatttggtgg atttgg                                         26


<210> SEQ ID NO 225
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
```

```
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 225

cccacctaca acaacaacac c                                              21


<210> SEQ ID NO 226
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 226

gaacgcgtac ggaaggtagg                                                20


<210> SEQ ID NO 227
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 227

gtgataggtt tgtagatttg atagttg                                        27


<210> SEQ ID NO 228
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 228

aactaacctc cattttaact atttc                                          25


<210> SEQ ID NO 229
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 229

gagagatgaa tttggatatt agt                                            23


<210> SEQ ID NO 230
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (14)..(14)
<223> OTHER INFORMATION: “y” may be “c” or “t”

<400> SEQUENCE: 230

ggtaaattgg tgtygttgga gaag                                           24


<210> SEQ ID NO 231
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (18)..(18)
```

-continued

```
<223> OTHER INFORMATION: "r" may be "a" or "g"

<400> SEQUENCE: 231

actaaacaat aatacccrac ctc                                             23


<210> SEQ ID NO 232
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Primer

<400> SEQUENCE: 232

gtcgttgggt tcggtttcgt tttg                                            24
```

The invention claimed is:

1. A method of determining the methylation status of one or more CpG islands indicative of prostate cancer in a human male undergoing prostate cancer evaluation, which method comprises:

isolating or amplifying genomic DNA from a biological sample from a human male undergoing prostate cancer evaluation; and

assaying the genomic DNA for methylation of one or more CpG islands including a CpG island in SEQ ID NO: 49 or SEQ ID NO: 50 associated with NODAL,

wherein the presence of the methylation of the one or more CpG islands, including the CpG island associated with NODAL, is indicative of prostate cancer.

2. The method of claim **1**, wherein the method further comprises assaying the isolated or amplified genomic DNA for methylation of one or more CpG islands associated with HEMK1, GPX7, PALD, or FGF20, and wherein the presence of the methylation of the one or more CpG islands associated with HEMK1, GPX7, PALD, or FGF20 is indicative of prostate cancer.

3. The method of claim **1**, wherein the method further comprises assaying the isolated or amplified genomic DNA for methylation of CpG islands associated with HEMK1, GPX7, PALD, and FGF20, and wherein the presence of the methylation of the CpG islands is indicative of prostate cancer.

4. The method of claim **1**, wherein the method further comprises assaying the isolated or amplified genomic DNA for methylation of a CpG island associated with at least one gene that is known to be methylated in prostate cancer and that is known not to be detectably methylated or methylated at a lower level in benign prostate hyperplasia (BPH), and wherein the presence or increased methylation of the assayed CpG islands is indicative of prostate cancer.

5. The method of claim **2**, wherein the method further comprises assaying the isolated or amplified genomic DNA for methylation of a CpG island associated with at least one gene that is known to be methylated in prostate cancer and that is known not to be detectably methylated or methylated at a lower level in benign prostate hyperplasia (BPH), wherein the presence or increased methylation of the assayed CpG islands is indicative of prostate cancer.

6. The method of claim **4**, wherein the CpG island associated with at least one gene that is known to be methylated in prostate cancer and that is known to be unmethylated or methylated at a lower level in BPH is or includes one or more CpG islands associated with glutathione S-transferase P1 (GSTP1), glutathione peroxidase 3 (GPX3), cyclin-dependent kinase inhibitor 1C (CDKN1C/p57), or G-protein coupled receptor 62 (GPR62).

7. The method of claim **4**, wherein the CpG island associated with at least one gene that is known to be methylated in prostate cancer and that is known to be unmethylated or methylated at a lower level in BPH includes a CpG island associated with glutathione S-transferase P1 (GSTP1).

8. The method of claim **1**, wherein the method further comprises assaying the isolated or amplified genomic DNA for methylation of at least one CpG island associated with a gene selected from the group consisting of kinesin family member 13B (KIF13B), neurogenin 3 transcription factor (NEUROG3), L-threonine dehydrogenase (TDH), N-acylsphingosine amidohydrolase (acid ceraminase) 1 (ASAH1), Kinesin family member C2 (KIFC2), GDNF family receptor alpha 1 (GFRA1), Dickkopf homolog 2 (DKK2), Ras association (Ra1GDS/AF-6) domain family 5 (RASSF5), tumor necrosis factor superfamily member 11 (TNFSF11), and leucine rich repeat containing 49 (LRRC49), and wherein the presence of the methylation of the CpG islands is indicative of prostate cancer.

9. The method of claim **4**, wherein the method further comprises assaying the isolated or amplified genomic DNA for methylation of at least one CpG island associated with a gene selected from the group consisting of kinesin family member 13B (KIF13B), neurogenin 3 transcription factor (NEUROG3), L-threonine dehydrogenase (TDH), N-acylsphingosine amidohydrolase (acid ceraminase) 1 (ASAH1), Kinesin family member C2 (KIFC2), GDNF family receptor alpha 1 (GFRA1), Dickkopf homolog 2 (DKK2), Ras association (Ra1GDS/AF-6) domain family 5 (RASSF5), tumor necrosis factor superfamily member 11 (TNFSF11), and leucine rich repeat containing 49 (LRRC49), and wherein the presence of the methylation of the CpG islands is indicative of prostate cancer.

10. The method of claim **8**, wherein the method comprises assaying for methylation of CpG islands associated with at least 7 genes.

11. The method of claim **8**, wherein the method comprises assaying for methylation of CpG islands associated with at least 8 genes.

12. The method of claim **8**, wherein the method comprises assaying for methylation of CpG islands associated with at least 9 genes.

13. The method of claim **1**, wherein the assaying for methylation of a CpG island comprises amplifying a target sequence that includes a CpG island in SEQ ID NO: 49 or SEQ ID NO: 50.

14. The method of claim **8**, wherein the assaying for methylation of the at least one CpG island associated with a gene comprises amplifying a target sequence that includes at least one CpG island in sequence selected from the group consisting of (a) SEQ ID NOs: 7 or 8 [KIF13B], SEQ ID NOs: 13 or 14 [NEUROG3], SEQ ID NOs: 35 or 36 [TDH], SEQ ID NOs: 43 or 44 [ASAH1], SEQ ID NOs: 119 or 220 [KIFC2], SEQ ID NOs: 123 or 124 [GFRA1], SEQ ID NOs: 129 or 130 [DKK2], SEQ ID NOs: 133 or 134 [RASSF5], SEQ ID NO: 196 [TNFSF11], and SEQ ID NO: 198 [LRRC49], and (b) fully or partially methylated sequences of (a).

15. The method of claim **1**, wherein assaying the genomic DNA for methylation comprises terminator-coupled linear amplification.

16. The method of claim **1**, wherein assaying the genomic DNA for methylation comprises using methylation-sensitive restriction endonuclease.

17. The method of claim **1**, wherein assaying the genomic DNA for methylation comprises differential methylation hybridization.

18. The method of claim **1**, wherein the amplification of genomic DNA comprises methylation coupled genomic amplification.

19. The method of claim **1**, wherein assaying the genomic DNA for methylation comprises quantitative PCR.

20. The method of claim **1**, wherein assaying the genomic DNA for methylation comprises sequencing.

21. The method of claim **1**, wherein the biological sample is whole blood, blood plasma, or blood serum.

22. The method of claim **1**, wherein the biological sample is urine.

23. The method of claim **1**, wherein the biological sample is prostate tissue.

24. The method of claim **2**, wherein the method comprises assaying the isolated or amplified genomic DNA for methylation of one or more CpG islands in SEQ ID NO: 17 or 18 [HEMK1], SEQ ID NOs: 125 or 126 [GPX7], SEQ ID NO: 15 or 16 [PALD], or SEQ ID NO: 39 or 40 [FGF20], and wherein the presence of the methylation of the one or more CpG islands associated with HEMK1, GPX7, PALD, or FGF20 is indicative of prostate cancer.

* * * * *